

GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

Run on: March 26, 2003, 04:18:30 ; Search time 4821.31 Seconds
(without alignments)
15096.740 Million cell updates/sec

Title: US-09-702-134-7212_COPY_28000_30500
Perfect score: 2501
Sequence: 1 atgtccaagataaaattggc.....ctatcaatggttgcttcaat 2501

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

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2: gb.htg.*
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6: gb.pat.*
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Match	Length	DB	ID	Description
C	1	2501	100.0	145999	2	AC096690	Oryza sat
	2	2501	100.0	244803	2	AC128647	AC128647 Oryza sat
	3	1568.2	62.7	1598	8	OSU50333	U50333 Oryza sativ
	4	602.2	24.1	1451	8	TAY14009	Y14009 Triticum ae
	5	596.8	23.9	1343	8	AB005555	AB005555 Triticum ae
	6	596.8	23.9	1431	8	TAY14007	Y14007 Triticum ae
	7	590.6	23.6	1446	8	TAY14008	Y14008 Triticum ae
	8	586.4	23.4	1171	8	AY014280	AY014280 Lolium pe
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	13	367.6	14.7	1170	8	AY114310	AY114310 Oryza sat
	14	313.2	12.5	1513	8	PVU70531	U70531 Phaseolus v
	15	309	12.4	1511	8	AB012203	AB012203 Lactuca s
	16	299.4	12.0	1601	8	PVU70530	U70530 Phaseolus v
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	18	292.4	11.7	1259	6	A41577	A41577 Sequence 3
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	21	287.2	11.5	1857	8	PTXPTGIBB	AJ001326 Populus t
	22	282.2	11.3	1512	8	STU291453	AJ291453 Solanum t
	23	282.2	11.3	1629	8	FSY420192	AJ420192 Fagus syl
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	27	277.8	11.1	1539	8	SDU252088	AJ252088 Solanum d
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ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION Oryza sativa chromosome 3 clone OSUNBa0059G06, *** SEQUENCING IN
PROGRESS ***, 5 ordered pieces.
ACCESSION AC096690
VERSION AC096690.4 GI:20503077
KEYWORDS HTG; HTGS; PHASE2.
SOURCE Oryza sativa.
ORGANISM Oryza sativa.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 145999)
AUTHORS Buell,C.R., Yuan,Q., Ouyang,S., Liu,J., Tallon,L., Gansberger,K.,

Kim, M., Overton II, L., Bera, J., Tsitir, T., Krol, M., Jarrahi, B., Jin, S., Koo, H., Zismann, V., Hsiao, J., Blunt, S., Vanaken, S., Uterbach, T., Helblum, T., Haas, B., Sub, B., Peterson, J., Quackenbush, J., White, O., Salzberg, S. and Fraser, C.
Oryza sativa ssp. japonica cv. Nipponbare OSUNBa0059G06 BAC genomic sequence
Unpublished
2 (bases 1 to 145999)
Buell, R.
Direct Submission
Submitted (22-SEP-2001) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA
3 (bases 1 to 145999)
Buell, R.
Direct Submission
Submitted (08-MAY-2002) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA
On May 8, 2002 this sequence version replaced gi:19881803.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 5 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 1 3902: contig of 3902 bp in length
* 3903 4002: gap of unknown length
* 4003 71267: contig of 67265 bp in length
* 71268 71367: gap of unknown length
* 71368 94679: contig of 23312 bp in length
* 94680 94779: gap of unknown length
* 94780 122220: contig of 27441 bp in length
* 122221 122320: gap of unknown length
* 122321 145999: contig of 23679 bp in length.
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/db_xref="taxon:4530"
/chromosome="3"
/clone="OSUNBa0059G06"
/note="japonica cultivar-group"
BASE COUNT 40847 a 32003 c 31335 g 41412 t 402 others
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 115536 ATGTCCAGATAAATTTGGCCCAAGTGAAGAACTCAGAACTACATAAATAATTTTCGCA 115477
QY 61 ATGCCCAAACTATTTGGATGGTATTTGACGTGGGATCAGATCAGATCAGATCAG 120
Db 115476 ATGCCCAAACTATTTGGATGGTATTTGACGTGGGATCAGATCAGATCAGATCAG 115417
QY 121 AAAACCCATTTTACATATGATCTGTGAGGAGGCTGTGCAAACTGATTTTTCAG 180
Db 115416 AAAACCCATTTTACATATGATCTGTGAGGAGGCTGTGCAAACTGATTTTTCAG 115357
QY 181 CGAGCAAGTAAGACTTTTCGACTAGAACGATTTTATTTTAAAAAAGAAATAAAC 240
Db 115356 CGAGCAAGTAAGACTTTTCGACTAGAACGATTTTATTTTAAAAAAGAAATAAAC 115297
QY 241 TACAGATCCAGACCTATAGTAGGTAGCCGATGTGGCCGGCCGCTGTGGTCCGT 300
Db 115296 TACAGATCCAGACCTATAGTAGGTAGCCGATGTGGCCGGCCGCTGTGGTCCGT 115237
QY 301 TGGCTGGGTCAAGAGACAGATGGGCTAAGCAAAATACCGGTTGTGGCACCACCTTT 360
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Db 115236 TGCTGGGTACAAAGACAGAGAGTGGGCTAAGCAAAATACCGGTTGTGGCACCACCTTT 115177
QY 361 CACATTCACTCTCTCTTGTGATATCTTCTCTCATGGAAGAAAGAGATAGTAATTTTA 420
|||||
Db 115176 CACATTCACTCTCTTGTGATATCTTCTCTCATGGAAGAAAGAGATAGTAATTTTA 115117
QY 421 ATTGATCCGGGATAGAGAGAGAGAGAGATTAAAGAGGTAGCTAGGGAGAGAGCGAG 480
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Db 115116 ATTGATCCGGGATAGAGAGAGAGAGAGATTAAAGAGGTAGCTAGGGAGAGAGCGAG 115057
QY 481 TTGATCCCTGTGATCGATCGATCTGTGGCGCAGCGTGTATATAGGCGCGGAGG 540
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Db 115056 TTGATCCCTGTGATCGATCGATCTGTGGCGCAGCGTGTATATAGGCGCGGAGG 114997
QY 541 GAGTGAGAGAGACAGCAGCTAGCTAGCCGCGCTGGTCCAGCTGCTGGGGATGAG 600
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Db 114996 GAGTGAGAGAGACAGCAGCTAGCTAGCCGCGCTGGTCCAGCTGCTGGGGATGAG 114937
QY 601 TACTTAGTTCGGAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAG 560
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Db 114936 TACTTAGTTCGGAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAG 114877
QY 661 ACAGTTATTAGTTAGTTAGTTAGTTAGTTAGTTAGTTAGTTAGTTAGTTAGTTAG 720
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Db 114876 ACAGTTATTAGTTAGTTAGTTAGTTAGTTAGTTAGTTAGTTAGTTAGTTAG 114817
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Db 114816 GATAGTATTATCAACAATTAATAGCATGGTGGTGACAGAGAGAGAGAGTGGTGT 114757
QY 781 TCAGCGCGGGTGTGAGCGGGGACAGAGATCCGTCGCGAGTTATATATGCGCGCGG 840
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Db 114756 TCAGCGCGGGTGTGAGCGGGGACAGAGATCCGTCGCGAGTTATATATGCGCGCGG 114697
QY 841 AGAGAGACCCCGGGTCGGTGGCGGTGGAGAGCTGGAGTGGCGCTGATCAGCTGGGG 900
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Db 114696 AGAGAGACCCCGGGTCGGTGGCGGTGGAGAGCTGGAGTGGCGCTGATCAGCTGGGG 114637
QY 901 CGGGGGGAGAGAGTGTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 960
Db 114636 CGGGGGGAGAGAGTGTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 114577
QY 961 TCTTCTGTGGTGTAAACACAGCATCGAGCGCGCTGCTGGAGAGAGCGCACCGTGTCA 1020
Db 114576 TCTTCTGTGGTGTAAACACAGCATCGAGCGCGCTGCTGGAGAGAGCGCACCGTGTCA 114517
QY 1021 TGGACGCTTTCTTCAGCTGGCGTGGGGGAGAGAGAGCGCGCGCGCGCGCGGGG 1080
Db 114516 TGGACGCTTTCTTCAGCTGGCGTGGGGGAGAGAGAGCGCGCGCGCGCGCGGGG 114457
QY 1081 AGAGCTCGGCTACGCCAGCAGCTTCACGGGGCGCTTCGCTCCAGCTCCGCTGGAGG 1140
Db 114456 AGAGCTCGGCTACGCCAGCAGCTTCACGGGGCGCTTCGCTCCAGCTCCGCTGGAGG 114397
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Db 114336 AGTACCTGTGTCGGAAGCTTGGGGGAGAGAGAGCGCGCGCGCGCTGGCGAGTGTACT 114277
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QY 1321 TGGGATCTGTCGAGAGCGCGCGCTACTTCCGCGGATTTCTCCAGCGCAACACTTCCA 1380
Db 114216 TGGGATCTGTCGAGAGCGCGCGCTACTTCCGCGGATTTCTCCAGCGCAACACTTCCA 114157
QY 1381 TCATCGCCTCAACTACTACCGCGCTGCCAGAGCGCTGCCAGACGCTGGCGACCGCGTCC 1440
Db 114156 TCATCGCCTCAACTACTACCGCGCTGCCAGAGCGCTGCCAGACGCTGGCGACCGCGTCC 114097

QY	1441	CGCACTCGGACGCCACCTCGCTCAACATCCTCCACACGAGGACACGTCGCGCGCGCTGGAGG	1500
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RESULT 2	AC128647	244803 bp	DNA	linear	HTG 20-JUL-2002
LOCUS	Orzya sativa	chromosome 3 clone OSUNB0062G19	*** SEQUENCING IN		
DEFINITION	PROGRESS ***	33 unordered pieces.			
ACCESSION	AC128647	GI:21913026			
VERSION	AC128647.1	GTGS-PHASE1.			
KEYWORDS	HTG; HTGS-PHASE1.				
SOURCE	Orzya sativa				
ORGANISM	Orzya sativa				
REFERENCE	Enkaryota: Viridiplantae: Streptophyta; Embryophyta: Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Focaceae; Ehrhartoidae; Orzyaceae; Orzya.				
AUTHORS	1 (bases 1 to 244803)				
REFERENCES	Buell, C.R., Yuan, Q., Ouyang, S., Liu, J., Tallon, L., Gansberger, K., Kim, M., Overton I.L., Bera, J., Tsitrin, T., Krol, M., Jarrahi, B., Jin, S., Koo, H., Zismann, V., Hsiao, J., Blunt, S., Vanaken, S., Utterbach, T., Feldblyum, T., Yang, Q., Haas, B., Suh, B., Peterson, J., Quackenbush, J., White, O., Salzberg, S. and Fraser, C.				
TITLE	Orzya sativa ssp. japonica cv. Nipponbare OSUNB0062G19 BAC genomic sequence				
JOURNAL	Unpublished				
REFERENCE	2 (bases 1 to 244803)				
AUTHORS	Buell, R.				
TITLE	Direct Submission				
JOURNAL	Submitted (20-JUL-2002) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA				
COMMENT	* NOTE: This is a 'working draft' sequence. It currently consists of 33 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.				
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	188346	188393: gap of unknown length			
	188394	193528: contig of 5135 bp in length			

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* 210166 212168: contig of 2003 bp in length
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* 212217 216130: contig of 3914 bp in length
* 216131 218511: contig of 2333 bp in length
* 218512 218559: gap of unknown length
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* 221032 221079: gap of unknown length
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* 229779 229826: gap of unknown length
* 229827 232767: contig of 2941 bp in length
* 232768 232815: gap of unknown length
* 232816 235017: contig of 2202 bp in length
* 235018 235065: gap of unknown length
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2501; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 108917 AAAACCATTTTACATATGATCTGTGTAGGAGGCTGCTTCCAAAATGATTTTTCGAG 108976

QY 181 GCAGGCAAGTAAAGCTTTCAGTACAGCAATTTTTTTTTTAAATAAAGATAACAC 240
Db 108977 GCAGGCAAGTAAAGCTTTCAGTACAGCAATTTTTTTTTTAAATAAAGATAACAC 109036

QY 241 TACAGATCCAAAGACCTATAGTATAGGCTAAGCCGATGTGGCCGGCGGCTGTGGTCCGT 300
Db 109037 TACAGATCCAAAGACCTATAGTATAGGCTAAGCCGATGTGGCCGGCGGCTGTGGTCCGT 109096

QY 301 TGGCTGGGTACAAAGACAGAGTGGGTAAAGCAATACCGGTTGTGGCAATCCCTTT 360
Db 109097 TGGCTGGGTACAAAGACAGAGTGGGTAAAGCAATACCGGTTGTGGCAATCCCTTT 109156

QY 361 CACATTCACCTCGCTTGTATATCTTCTCTCATGTGAAAAGAGAGATAAGTAATTTTA 420
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QY 421 ATTGATCCGGGTATAGAGACAGAGAGACTTAAGAGTACTAGGCGGAGGAGCGAG 480
    
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 VERSION
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 wga20.
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 Poideae; Triticeae; Triticum.
 Youssefian,S.
 Characterization of a gibberellin 20-oxidase gene from wheat and
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 Unpublished
 2 (bases 1 to 1343)
 Youssefian,S.
 Direct Submission
 Submitted (04-JUL-1997) Shohab Youssefian, Akita Prefectural
 College of Agriculture, Biotechnology Institute; 2-2 Minami,
 Oogataura, Minamiakita-gun, Akita 010-04, Japan
 (E-mail:shohab@akita-u.ac.jp, Tel:0185-45-2026,
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ORIGIN

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RESULT 12
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 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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 Ehrhartoideae; Oryzaceae; Oryza.
 REFERENCE 1
 AUTHORS Sasaki,A., Ashikari,M., Ueguchi-Tanaka,M., Itoh,H., Nishimura,A.,
 Swapan,D., Ishiyama,K., Saito,T., Kobayashi,M., Khush,G.S.,
 Kitano,H. and Matsuo,M.
 Green revolution: A mutant gibberellin-synthesis gene in rice
 Nature 416 (6882), 701-702 (2002)
 JOURNAL NATURE 416 (6882), 701-702 (2002)
 MEDLINE 21959433
 PUBMED 11961544
 REFERENCE 2 (bases 1 to 1170)
 AUTHORS Matsuo,M., Sasaki,A. and Ashikari,M.
 TITLE Direct Submission
 JOURNAL Submitted (25-DEC-2001) Makoto Matsuo, Nagoya University,
 Bioscience Center, Furocho, Chikusa, Nagoya, Aichi 464-8601, Japan
 (E-mail:makoto@nuagr1.agr.nagoya-u.ac.jp, Tel:81-52-789-5225,
 Fax:81-52-789-5226)

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DEFINITION			
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AUTHORS			
TITLE			
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MEDLINE			
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REFERENCE	2	(bases 1 to 1513)
AUTHORS	Garcia-Martinez,J.L., Lopez-Diaz,I., Sanchez-Beltran,M.J., Phillips,A.L., Ward,D.A., Gaskin,P. and Hedden,P.	
TITLE	Direct Submission	
JOURNAL	Submitted (12-SEP-1996) Instituto de Biologia Molecular y Celular de Plantas, Universidad Politecnica/CSIC, Camino de Vera s/n, Valencia 46022, Spain	
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 Job time : 5400.98 secs

GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

Run on: March 26, 2003, 04:18:30 ; Search time 4242.99 Seconds
(without alignments)
15096.740 Million cell updates/sec

Title: US-09-702-134-7212_COPY_10200_12400

Perfect score: 2201

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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c 2	2201	100.0	244803	2	AC128647	AC128647 Oryza sat
c 3	2034.6	92.4	207376	2	AC104433	AC104433 Oryza sat
c 4	191.2	8.7	110969	2	CNS08C70	AL731741 Oryza sat
c 5	190.6	8.7	142475	8	AP003627	AP003627 Oryza sat
c 6	190.6	8.7	153449	8	AP003238	AP003238 Oryza sat
c 7	189.8	8.6	163279	8	AC078829	AC078829 Oryza sat
c 8	188.6	8.6	113825	2	OSUN00196	AL662998 Oryza sat
c 9	186.8	8.5	164852	2	AC092075	AC092075 Oryza sat
c 10	186.4	8.5	158805	2	AC104847	AC104847 Oryza sat
c 11	186	8.5	169663	2	CNS07VEX	AL713952 Oryza sat
c 12	185.6	8.4	91552	6	AX429455	AX429455 Sequence
c 13	185.4	8.4	148441	2	AP004691	AP004691 Oryza sat
c 14	185.2	8.4	154494	2	AC120885	AC120885 Oryza sat
c 15	184.6	8.4	179486	2	AP005305	AP005305 Oryza sat
c 16	184	8.4	172468	2	AP005589	AP005589 Oryza sat
c 17	183.8	8.4	129052	2	AP003754	AP003754 Oryza sat
c 18	183.4	8.3	134518	2	OSJN00134	AL662944 Oryza sat
c 19	183.4	8.3	141428	2	AP005558	AP005558 Oryza sat
c 20	183.2	8.3	124576	2	AP004078	AP004078 Oryza sat
c 21	183.2	8.3	172159	2	AP005492	AP005492 Oryza sat
c 22	183	8.3	133595	2	AC129227	AC129227 Oryza sat
c 23	183	8.3	160174	2	AP005103	AP005103 Oryza sat
c 24	183	8.3	170000	2	OSJN00133	AL662943 Oryza sat
c 25	182.8	8.3	121799	8	OSUN00064	AL666609 Oryza sat
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c 34	181.6	8.3	170025	2	OSJN00031	AL666590 Oryza sat
c 35	181.2	8.2	156829	2	AC120532	AC120532 Oryza sat
c 36	181	8.2	167379	2	AP004236	AP004236 Oryza sat
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c 41	180.4	8.2	152799	2	AC120539	AC120539 Oryza sat
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ALIGNMENTS

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VERSION AC096690.4 GI:20503077
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 145999)
AUTHORS Buell,C.R., Yuan,Q., Ouyang,S., Liu,J., Tallon,L., Gansberger,K.,


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* 232768 232815: gap of unknown length
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* 235018 235065: gap of unknown length
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QY 1741 CGGTGAGGAGGCGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1800
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RESULT 4
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 KEYWORDS Oryza sativa.
 SOURCE Oryza sativa.
 ORGANISM Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 REFERENCE 1 (bases 1 to 110969)
 AUTHORS Choise N., Orjeda G., Cattolico L., Demange N., Wincker P.,
 Seguren B., Pelletier E., Scarpelli C., Salanoubat M.,
 Weissenbach J. and Quetier F.
 TITLE Oryza sativa chromosome 12 sequencing
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 110969)
 AUTHORS Genoscope.
 JOURNAL Direct Submission
 TITLE Submitted (29-APR-2002) Genoscope - Centre National de Sequencage :
 BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
 - Web : www.genoscope.cns.fr)
 COMMENT IMPORTANT: This sequence is unfinished and does not necessarily
 represent the correct sequence.
 Work on the sequence is in progress and the release of this data is
 based on the understanding that the sequence may change as work
 continue. The sequence may be contaminated with foreign sequence
 from E.coli, yeast, vector, phage, etc.
 The nucleotide sequence of this BAC clone was generated by
 combining Monsanto and Genoscope sequencing data.
 Contigs composition :
 2400 bp contig from 1 to 2400
 8009 bp contig from 2501 to 8509
 5450 bp contig from 8610 to 14059
 11245 bp contig from 14160 to 25404
 85465 bp contig from 25505 to 110969.
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 5 contigs. Gaps between the contigs
 * are represented as runs of N. The order of the pieces
 * is believed to be correct as given, however the sizes
 * of the gaps between them are based on estimates that have
 * provided by the submittor.
 * This sequence will be replaced
 * by the finished sequence as soon as it is available and
 * the accession number will be preserved.
 * 1 2400: contig of 2400 bp in length
 * 2401 2500: gap of 100 bp
 * 2501 8509: contig of 6009 bp in length
 * 8510 8609: gap of 100 bp
 * 8610 14059: contig of 5450 bp in length
 * 14060 14159: gap of 100 bp
 * 14160 25404: contig of 11245 bp in length
 * 25405 25504: gap of 100 bp
 * 25505 110969: contig of 85465 bp in length.
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 /sub_species="japonica"
 /db_xref="taxon:4530"
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 /clone_lib="Monsanto"
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 ORIGIN
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 Best Local Similarity 88.1%; Pred. No. 8.1e-23;
 Matches 222; Conservative 0; Mismatches 23; Indels 7; Gaps 1;
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Db 95874 TTATAGCCTCATATTTTAAATGATGACACCGTTGACTTTTGTCCACGTTTGACCAATT 95933
 QY 902 COTCTTATTAATAAAAAATTATGATCATCTATTATTATTATTATTATGACTTTGATCGTCATC 961
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 QY 1075 TATGGGATAGCT 1086
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 Db 96114 TATGGTGTAGCT 96125
 RESULT 5
 AP003627 142475 bp DNA linear PLN 21-MAR-2002
 LOCUS Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1,
 DEFINITION PAC clone:P0459B04.
 ACCESSION AP003627
 VERSION AP003627.3 GI:15290128
 KEYWORDS
 SOURCE Oryza sativa (japonica cultivar-group) (cultivar:Nipponbare) DNA,
 clone:P0459B04.
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 REFERENCE 1
 AUTHORS Sasaki,T., Matsumoto,T. and Yamamoto,K.
 TITLE Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
 clone:P0459B04
 JOURNAL Published Only in Database (2001)
 REFERENCE 2 (bases 1 to 142475)
 AUTHORS Sasaki,T., Matsumoto,T. and Yamamoto,K.
 TITLE Direct Submission
 JOURNAL Submitted (17-MAY-2001) Takuji Sasaki, National Institute of
 Agrobiological Sciences, Rice Genome Research Program; Kannondai
 2-1-2, Tsukuba, Ibaraki 305-8602, Japan
 (E-mail:tsasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/,
 Tel:81-298-38-7441, Fax:81-298-38-7468)
 On Aug 24, 2001 this sequence version replaced gi:14575596.
 Genes were predicted from the integrated results of the following:
 GENSCAN1.0, BLASTN2.0, BLASTX2.0 as well as SplicePredictor
 (October 1998 version). The genomic sequence was searched against
 NCBI NonRedundant Protein database, nr
 (ftp://ncbi.nlm.nih.gov/blast/db) and the cDNA sequence database at
 RGP. Protein homologies of the coding regions were searched against
 NCBI NonRedundant Protein database with BLASTP2.0. ESTs represent
 the identified cDNA sequences using BLASTN 2.0 with the
 corresponding DDBJ accession no. and RGP clone ID.
 A gene with identity or significant homology to a protein is
 classified based on the protein name to indicate the homology level
 such as same name, 'putative-' and '-like protein'. A gene without
 significant homology to any protein but with EST homology (covering
 almost the entire length of partial sequence) is classified as an
 'unknown' protein. A gene predicted with a gene prediction program
 is classified as a 'hypothetical' protein.
 The orientation of the sequence is from SP6 to T7 of the PAC clone.
 Detailed information on overlap and assembly quality together with
 annotation of this entry is available at
 http://rgp.dna.affrc.go.jp/GenomesSeq.html.
 FEATURES Location/Qualifiers
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 /db_xref="taxon:39947"
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HFIDQDLDRVGGVDIICLEYSRANSREKRDLFVLFDYVLIHQINEFLAGLSITYY
DDAQLASILACADAPAFYISVKGHVEGVDMLRAISSALSSALSTETEQNLVLDKV
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AWGADRLQDSAGRIAYAVMRGRACAAALNPAAP IVPSPLEITGELADAKA
LLEAALNREKRIKLGSDINIKGDEEESDEEACNICPEOACMEYKEGCH
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FEATURES	source
gene	This sequence of P0698H10 clone has an overlap with P0518C01 (DDBJ: AP003277) clone at the position 1 to 80,700 of 5' end and with P0459B04 (DDBJ: AP003627) at the position 103,851 to 153,449 of 3' end. Detailed information on overlap and assembly quality together with annotation of this entry is available at http://gfp.dna.affro.go.jp/GenomeSeq.html .
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Db 148280 CATTGCTCTTATTAATAAATAATATGATCTATCTATTTATTTATTTATGATGATTCGTT 148339
QY 958 CATCAATATTTTAAAGCATGACATAAACAATTTTCATATTTTGCACAAA-----AAAA 1010
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DEFINITION complete sequence.
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VERSION AC078829.10 GI:21686922
KEYWORDS HTG.
SOURCE Oryza sativa (japonica cultivar-group).
ORGANISM Oryza sativa (japonica cultivar-group)
Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 163279)
Buell,C.R., Yuan,Q., Moffat,K.S., Hill,J.N., Burr,P.C., Hsiao,J.,
Zismann,V., Pal,G., Bowman,C.L., Fujii,C.Y., VanNaken,S.E.,
Bowman,C.L., Craven,B., Utterback,T.R., Khalak,H., Feldblyum,T.V.,
Quackenbush,J., White,O., Salzberg,S.L. and Fraser,C.M.
Oryza sativa chromosome 10 BAC OSJNBa0026012 genomic sequence
Unpublished
2 (bases 1 to 163279)
Buell,R.
Direct Submission
Submitted (04-AUG-2000) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA
3 (bases 1 to 163279)
Buell,R.
Direct Submission
Submitted (27-FEB-2001) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA, rbuella@igr.org
4 (bases 1 to 163279)
Buell,R.
Direct Submission
Submitted (13-MAR-2001) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA, rbuella@igr.org
5 (bases 1 to 163279)
```

AUTHORS

Buell, R.

TITLE

Direct Submission

JOURNAL

Submitted (29-AUG-2001) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA, rbuelli@tigr.org
6 (bases 1 to 163279)

AUTHORS

Buell, R.

TITLE

Direct Submission

JOURNAL

Submitted (03-JUL-2002) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA, rbuelli@tigr.org
On Jul 3, 2002 this sequence version replaced gi:13129494.
Address all correspondence to:rice@tigr.org

COMMENT

BAC clone OSJNBa0026012 is from Oryza sativa chromosome 10.
The orientation of the sequence is from SP6 to P7 end of the BAC
clone.

Genes were identified by a combination of several methods: Gene
prediction programs including Genscan and Genscan+ (Chris Burge,
<http://CCR-081.mit.edu/GENSCAN.html>), GeneMarkHM (Mark Borodovsky,
<http://genemark.biology.catech.edu/GeneMark/>), Fgenesh
(<http://www.softberry.com/>), and GeneSplicer (Minaelja Perteza and
Steven Salzberg, contact.mperetea@tigr.org), searches of the
complete sequence against a peptide database and the plant EST
database at tigr (<http://www.tigr.org/tdb/tgi.shtml>). Annotated
genes are named to indicate the level of evidence for their
annotation. Genes with similarity to other proteins are named after
the database hits. Genes without significant peptide similarity but
with EST similarity are named as unknown proteins. Genes without
protein or EST similarity, that are predicted by more than two gene
prediction programs over most of their length are annotated as
hypothetical proteins. Genes encoding tRNAs are predicted by
tRNAscan-SE (Sean Eddy, <http://genome.wustl.edu/eddy/tRNAscan-SE/>).
Simple repeats are identified by repeatmasker (Arian Smit,
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>).

This BAC overlaps with rice BAC OSJNBb0044B19 (AC078893) and
OSJNBa005P24 (AC037425).

FEATURES

source

Location/Qualifiers

1..163279
/organism="Oryza sativa (japonica cultivar-group)"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/chromosome="10"
/map="B3243"
/clone="OSJNBa0026012"

/note="japonica cultivar-group"

complement(1575..1683)

/rpt_family="AT-rich"

1643..1669

/rpt_family="(TA)n"

complement(2060..2100)

/rpt_family="AT-rich"

complement(2700..2723)

/rpt_family="AT-rich"

complement(5159..5181)

/rpt_family="AT-rich"

complement(6896..6927)

/rpt_family="AT-rich"

complement(11673..11753)

/rpt_family="AT-rich"

complement(13043..13081)

/rpt_family="AT-rich"

complement(16661..16686)

/rpt_family="AT-rich"

complement(18032..18065)

/rpt_family="AT-rich"

complement(26795..29035)

/gene="OSJNBa0026012.16"

/note="similar to nuclear

GI:4803672 (Homo sapiens)"

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27721..27783,27886..27963,28907..>29035))

/gene="OSJNBa0026012.16"

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27721..27783,27886..27963,28907..29035))

/gene="OSJNBa0026012.16"

/codon_start=1

/product="putative nuclear transport receptor"

/protein_id="AAK13152.1"

/db_xref="GI:13129498"

/translation="MEQATAAVKAALAAALVHHDDATTAADRWLQQPQHTLDAQV
ADSLHDESSNMETQIFCSQTKRSQVDFEELPSEAFRLQSLYALKKFSKGPQK
VNTQICAMALAVHFFG"
29166..29196

/rpt_family="(TGGGG)n"

complement(29966..30049)

/rpt_family="AT-rich"

33907..33945

/rpt_family="(CGG)n"

complement(34290..34356)

/rpt_family="(TA)n"

34452..34525

/gene="OSJNBa0026012.LRNA-Asn-1"

34452..34525

/gene="OSJNBa0026012.LRNA-Asn-1"

/product="tRNA-Asn"

complement(35292..35312)

/rpt_family="AT-rich"

complement(36223..37996)

/gene="OSJNBa0026012.6"

/note="similar to NAM GB:CAA63101 GI:1279640 (Petunia x

hybrida)"

complement(join<36223..36759,36892..37157,37825..>37996))

/gene="OSJNBa0026012.6"

complement(join(36223..36759,36892..37157,37825..37996))

/gene="OSJNBa0026012.6"

/codon_start=1

/product="putative NAM (no apical meristem) protein"

/protein_id="AAK13151.1"

/db_xref="GI:13129497"

/translation="MAGLEMESTLPPGFRCPDSEELICFYLKNKVANHRVASGLV
DYDLHAREPLPEAKLAEWIFFSFDRKIATGRTNRAKTGWKATGNDRIHV
EGTTRAVVGMKTLVFLYGLRAPNGKQTTWVHEFRLFTPSQPKEDWLCRVDFKKP
STIEAEGGGSGSLDFIPGATGSDPSPSTPTMAPLLGSPDPTVYDFRHSAAVPP
LNVLMGGGDOMTALMGCGFEGHGRILEMEPAWRQGGGNCVRYELF"

complement(40273..40295)

/rpt_family="AT-rich"

41836..56291

/rpt_family="Oryza sativa gene, repeat sequence Micropon-4

gi|4586620|dbj|AB010112.1|AB010112"

complement(41836..41884)

/rpt_family="(TA)n"

41837..56287

/rpt_family="Oryza sativa gene, repeat sequence Micropon-4

gi|4586620|dbj|AB010112.1|AB010112"

41839..56317

/rpt_family="Oryza sativa gene, repeat sequence Micropon-4

gi|4586620|dbj|AB010112.1|AB010112"

complement(41839..56317)

/rpt_family="Oryza sativa gene, repeat sequence Micropon-4

gi|4586620|dbj|AB010112.1|AB010112"

41839..47540

/rpt_family="Oryza sativa gene, repeat sequence Micropon-3

gi|4586621|dbj|AB010113.1|AB010113"

complement(42556..42578)

/rpt_family="AT-rich"

complement(43917..43952)

/rpt_family="AT-rich"

44435..44459

/rpt_family="(GA)n"

complement(44595..44665)

/rpt_family="AT-rich"

complement(47490..47539)

/rpt_family="(TA)n"

complement(48654..48681)

/rpt_family="(GA)n"

```

CHINA. E-mail enquiries: bhan@ncgr.ac.cn. Clone requests:
bhan@ncgr.ac.cn
Oryza sativa japonica (nipponbare) genomic DNA, chromosome 4, BAC
clone: OSJNB0020011.
On Jul 12, 2002 this sequence version replaced gi:1798510.
Web site: http://www.ncgr.ac.cn
----- Summary Statistics -----
Assembly program: phrap

NOTE: This is a PHASE2 sequence. Gaps are shown by nnnn. Genes
were identified by a combination of several methods: Gene
identification programs including Fgenesh (http://www.softberry.com/),
genscan (http://CCR-091.mit.edu/GENSCAN.html), GenemarkHMM
(http://genemark.biology.gatech.edu/Genemark/), TRNAScan-SE (Sean
Eddy, http://genome.wustl.edu/eddy/TRNAScan-SE/), searches of the
complete sequence against NCBI non-redundant protein database (nr)
(http://ncbi.nlm.nih.gov/blast/db) and the EST database at NCGR.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces

```

* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* been provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
*
* 1 88356: contig of 88356 bp in length
* 88357 88556: gap of 200 bp
* 88557 113825: contig of 25269 bp in length.

QY	843	TACTACCTCCATATTTTAAATGATGAGCGCGTTGACATTTTGTCCACAGGTTTGACCATTC	902
Db	101222	TACTATCTCCATATTTTAAATGATGAGCGCGTTGACATTTTGTCCACAGGTTTGACCATTC	101163
QY	903	GGCTTATTAAAAAAAATATGATCATATTTATTTATTTTATATGACTTGATCGTCATCA	962
Db	101162	GGCTTATTCAAAAAATTTANGTAATTAATCATTTTATTTATGACTTGATGATCATCA	101103
QY	963	AAATATTTTAAAGCATGACATAAAGATTTTCATATTTGCAAAAAAAA-----AAAAG	1015
Db	101102	AAATATCTTTTAAAGCATAAACATAAATATTTTCATATTTGACAAAAATTTGAAATAAAG	101043
QY	1016	AATGGTGCAATGTTTAGTGCAAAAGTCATGGTGTCATACATTAAAAATGACGGAGGATTAT	1075
Db	101042	AATGGTCAAAGCTGGTGTGAAGGTCAACAGCGTCATACATTTAAATATGAGGGAGTAT	100983
QY	1076	ATGGGATAGCTACAGTAGCAGAGTCATGATAAAAGTAGTAACT	1118
Db	100982	ATTTTATGGCTTAAAGGCCGCCCTAAATATATATATTTATTTT	100940

[illegible]

Db 33651 ACARAAATTTTGAATAAAGCATGGTCARATGTTGATCGAAAAAGTCACGGCGTCATAC 33592

QY 1055 ATTAAATACGAGGAGTA 1074

Db 33591 GTTAAATACGAGGAGTA 33572

RESULT 13

AP004691/c

LOCUS

DEFINITION Oryza sativa (japonica cultivar-group) chromosome 8 clone P0453D01, linear HTG 21-MAR-2002

*** SEQUENCING IN PROGRESS ***

ACCESSION AP004691.1 GI:18447950

VERSION HTG; HTGS_PHASE2.

KEYWORDS Oryza sativa (japonica cultivar-group) (cultivar:Nipponbare) DNA,

SOURCE clone:P0453D01.

ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1

AUTHORS Sasaki,T., Matsumoto,T. and Yamamoto,K.

TITLE Oryza sativa nipponbare(GA3) genomic DNA, chromosome 8, PAC

JOURNAL Published only in Database (2002)

AUTHORS Oryza sativa P0453D01

TITLE 2 (bases 1 to 148441)

JOURNAL Direct Submission

AUTHORS Sasaki,T., Matsumoto,T. and Yamamoto,K.

TITLE Submitted (30-JAN-2002) Takuji Sasaki, National Institute of

Agrobiological Sciences, Rice Genome Research Program; Kannondai

2-1-2, Tsukuba, Ibaraki 305-8602, Japan

(E-mail:tsasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/,

Tel:81-298-38-7441, Fax:81-298-38-7468)

NOTE: It currently consists of 1 contigs. Gaps between the contigs

are represented as runs of N. The order of the pieces is believed

to be correct as given, however the sizes of the gaps between them

are based on estimates that have provided by the submitter. This

sequence will be replaced by the finished sequence as soon as it is

available and the accession number will be preserved.

* NOTE: This is a 'working draft' sequence.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

FEATURES Location/Qualifiers

source

1..148441

/organism="Oryza sativa (japonica cultivar-group)"

/cultivar="Nipponbare"

/db_xref="taxon:39947"

/chromosome="8"

/clone="P0453D01"

BASE COUNT 42350 a 31475 c 33016 g 41500 t 100 others

ORIGIN

Query Match 8.4%; Score 185.4; DB 2; Length 148441;

Best Local Similarity 83.9%; Pred. No. 8.6e-22;

Matches 224; Conservative 0; Mismatches 36; Indels 7; Gaps 1;

QY 833 TATTACTATTATACCTGCATATTTTATGATGACGCGGTTCACCTTTTGTCCACGT 892

|||||

Db 103723 TGTGCTATATACCTGCATATTTTATGATGACGCGGTTCACCTTTTGTCCACGT 103664

|||||

QY 893 TTGACCATTCCTCTATTAATAAATAATATGATCTATTATTATTATTATGACTTGA 952

|||||

Db 103663 TTGACCATTCCTCTATTAATAAATAATATGATCTATTATTATTATTATGACTTGA 103604

|||||

QY 953 TTGCTCATCAATAATTTTAAAGCATGACATAAACAATTTTCATATTTGCAAAA 1006

|||||

Db 103603 TTCTTCATCAATAATTTTAAAGCATGACATAAACAATTTTCATATTTGCAAAAATTTT 103544

|||||

QY 1007 -AAAAAAGCATGCTCAATGTTAGTGAAGTCAATGCTCATACATTAATAATACG 1065

|||||

Db 103543 GAATAAAAGCATGCTCAATGTTAGTGAAGTCAATGCTCATACATTAATAATACG 103484

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QY 1066 GAGGATTATATCGGATACGTACAGTA 1092

|||||

Db 103483 GAGGAGTATGTTTTTCAATGATTA 103457

RESULT 14

AC120885

LOCUS

DEFINITION

Oryza sativa (japonica cultivar-group) chromosome 11 clone

Ba0042J05, *** SEQUENCING IN PROGRESS ***

ACCESSION AC120885

VERSION AC120885.1 GI:20531970

KEYWORDS HTG; HTGS_PHASE2.

SOURCE Oryza sativa (japonica cultivar-group).

ORGANISM Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE 1 (bases 1 to 154494)

AUTHORS Khurana,J.P., #Linton,E.W., #Messing,J., Mohanty,A., Bharti,A.K.,

Raghuvanshi,S., Khurana,P. and Tyagi,A.K.

TITLE Oryza sativa (japonica cultivar-group) chromosome 11 BAC clone

JOURNAL Unpublished

REMARK # The Plant Genome Initiative at Rutgers - Waksman Institute,

Rutgers University 190 Frelinghuysen Road, Piscataway, NJ 08873,

USA

REFERENCE 2 (bases 1 to 154494)

AUTHORS Khurana,J.P., #Linton,E.W., #Messing,J., Mohanty,A., Bharti,A.K.,

Raghuvanshi,S., Khurana,P. and Tyagi,A.K.

TITLE Direct Submission

JOURNAL Submitted (13-MAY-2002) Indian Initiative for Rice Genome

Sequencing, Department of Plant Molecular Biology, University of

Delhi South Campus, New Delhi, Delhi 110021, India

REMARK # The Plant Genome Initiative at Rutgers - Waksman Institute,

Rutgers University 190 Frelinghuysen Road, Piscataway, NJ 08873,

USA

COMMENT

* NOTE: This is a 'working draft' sequence. It currently

* consists of 7 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submitter.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

FEATURES Location/Qualifiers

source

1..154494

/organism="Oryza sativa (japonica cultivar-group)"

/cultivar="Nipponbare"

/sub_species="japonica cultivar-group"

/db_xref="taxon:39947"

/chromosome="11"

/clone="Ba0042J05"

BASE COUNT 44561 a 32837 c 31980 g 44505 t 611 others

ORIGIN

Query Match 8.4%; Score 185.2; DB 2; Length 154494;

Best Local Similarity 82.0%; Pred. No. 9.4e-22;

Matches 228; Conservative 0; Mismatches 43; Indels 7; Gaps 1;
QY 807 GTTCACGGAATAGTATATGGACCTATTACTATTACTACCTCCATATTTTAATGTAT 866
|||||
Db 144949 GATGATAGGCAAGTGAAGCAGCTGCTTTATTTTATTTACTACCTCCGATTTTAAATGCAT 145008
|||||
QY 867 GACGCCGTTACATTTTGTCCAAAGCTTGGACCACTTCCTTATTAATAAAAAAATATGTAT 926
|||||
Db 145009 GACGTCGTTGACATTTTCTCTAAGTTTGGACCATTCGCTCTATTCACAAAATTTATGTAA 145068
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QY 927 CTATTTATTTATTTATGACCTGATTCGTCATCAAAATTTTAAAGCATGACATAAA 986
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Db 145069 TTATCATTTTATTTATGACCTGATTTCTTTATCAATGTTCTTTAAAGCATGACATAAA 145128
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QY 987 CATTTTCATATTGCAAAA-----AAAAAACGAATGGTCAAAATGTTAGTCGAAAG 1039
|||||
Db 145129 TATTTTCATATTGCAAAAATTTTGAATAAACGAATGGTCAAAATGTTAGTCGAAAG 145188
|||||
QY 1040 TCAATGGTGTCAATATAAATACGGAGGATATAT 1077
|||||
Db 145189 TCAACGGCATCATACATATAAATACGGAGGAGTATAT 145226
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RESULT 15
AP005305/c
LOCUS
DEFINITION Oryza sativa (japonica cultivar-group) DNA linear HTG 31-MAY-2002
*** SEQUENCING IN PROGRESS ***; 3 ordered pieces.
ACCESSION AP005305
VERSION AP005305.1 GI:21280355
KEYWORDS HTG; HTGS_PHASE2.
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group) (cultivar:Nipponbare) DNA,
clone:P0024C06.
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1
Sasaki,T., Matsumoto,T. and Katayose,Y.
Oryza sativa nipponbare(GR3) genomic DNA, chromosome 8, PAC
clone:P0024C06
Published Only in Database (2002)
REFERENCE
Sasaki,T., Matsumoto,T. and Katayose,Y.
Direct Submission
Submitted (29-MAY-2002) Takuji Sasaki, National Institute of
Agrobiological Sciences, Rice Genome Research Program; Kannondai
2-1-2, Tsukuba, Ibaraki 305-8602, Japan
(E-mail:tsasaki@nias.affrc.go.jp, URL:http://rpp.dna.affrc.go.jp/,
Tel:81-298-38-7441, Fax:81-298-38-7468)
NOTE: It currently consists of 1 contigs. Gaps between the contigs
are represented as runs of N. The order of the pieces is believed
to be correct as given, however the sizes of the gaps between them
are based on estimates that have provided by the submitter. This
sequence will be replaced by the finished sequence as soon as it is
available and the accession number will be preserved.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 1 22904: contig of 22904 bp in length
* 22905 23080: gap of 176 bp
* 23081 23081: contig of 1 bp in length
* 23082 23186: gap of 105 bp
* 23187 179486: contig of 156300 bp in length.
FEATURES
Location/Qualifiers
1..179486
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/cultivar="Nipponbare"
/db_xref="taxon:39947"
/chromosome="8"
/clone="P0024C06"
BASE COUNT 50872 a 39291 c 39711 g 49023 t 589 others
ORIGIN
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Best Local Similarity 85.98; Pred.No.1.2e-24;
Matches 219; Conservative 0; Mismatches 29; Indels 7; Gaps 1;
QY 834 ATTACTTATTACTACCTCCATATTTTAAATGATGACGCGTTCACCTTTTGTCCAAAGTT 893
|||||
Db 15016 ATTATTTGTTACTCCCTCCATATTTTAAATGATGACGCGTTCACCTTTTATCCAAATAT 14957
|||||
QY 894 TGACCATTCGCTCTTATTAATAAAAAATTAATGATCTATTTATTTATTTATGACTTGAT 953
|||||
Db 14956 TGACCATTCGCTCTTATTAATAAAAAATTTATGATCTATTTATTTATTTATGACTTGAT 14897
|||||
QY 954 TCGTCATCAATATTTTAAAGCATGACATAAAACATTTTCATATTTGCAAAAAA--- 1009
|||||
Db 14896 TTATCATCAAAATATTCCTTAAGCATGACATAAATATCTCATATTTGCAAAAAAATTTG 14837
|||||
QY 1010 ---AAAAAGATGGTCAAAATTTTAAAGTTCGAAAAAGTCAATGGTGTCTATACATTTAAATAACGG 1066
|||||
Db 14836 AATAAAATGAATGATCAAAACGTTGGTCAAAAAAGTCAACGACGTCATACATTAATAATACGG 14777
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QY 1067 AGGCAATATATGGGA 1081
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Db 14776 AGGAGATATCTAGAA 14762
|||||

Search completed: March 26, 2003, 14:00:53
Job time : 7637.65 secs

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 25, 2003, 18:27:39 ; Search time 335.492 Seconds
(without alignments)
14774.266 Million cell updates/sec

Title: US-09-702-134-7212_COPY_10200_12400
Perfect score: 2201
Sequence: 1 cgccttggtttgtgcatc.....tagcttggtttgtgta 2201

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_101002.*
1: /SID22/gcgdata/geneseq/geneseq-emb1/NA1980.DAT.*
2: /SID22/gcgdata/geneseq/geneseq-emb1/NA1981.DAT.*
3: /SID22/gcgdata/geneseq/geneseq-emb1/NA1982.DAT.*
4: /SID22/gcgdata/geneseq/geneseq-emb1/NA1983.DAT.*
5: /SID22/gcgdata/geneseq/geneseq-emb1/NA1984.DAT.*
6: /SID22/gcgdata/geneseq/geneseq-emb1/NA1985.DAT.*
7: /SID22/gcgdata/geneseq/geneseq-emb1/NA1986.DAT.*
8: /SID22/gcgdata/geneseq/geneseq-emb1/NA1987.DAT.*
9: /SID22/gcgdata/geneseq/geneseq-emb1/NA1988.DAT.*
10: /SID22/gcgdata/geneseq/geneseq-emb1/NA1989.DAT.*
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23: /SID22/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24: /SID22/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
c 1	185.6	8.4	91552	24 AAD38803
2	125.2	5.7	807	21 AAC52171
c 3	124.4	5.7	356	24 ABQ85736
4	124.4	5.7	1126	21 AAC47067
5	111.2	5.1	4569	24 ABK15663
6	110.2	5.0	689	24 ABQ85731
7	106.6	4.8	5241	21 AAA99467
8	101	4.6	7175	19 AAV35027
c 9	100	4.5	33675	24 AAD31202

c 10	100	4.5	69300	24 AAD38804
c 11	98.6	4.5	4569	24 ABK15663
12	98.2	4.5	91552	24 AAD38803
13	95.4	4.3	694	21 AAC48763
14	95.4	4.3	695	21 AAC44265
15	91.4	4.2	1591	18 AAT93780
c 16	90.8	4.1	6901	15 AAQ73703
17	84.6	3.8	1032	21 AAC44276
c 18	80.8	3.7	2317	20 AAX33532
c 19	80.6	3.7	5241	21 AAA99467
20	74.6	3.4	1978	20 AAX32597
21	72.6	3.3	33675	24 AAD31202
c 22	70.2	3.2	7175	19 AAV35027
c 23	68.4	3.1	1978	20 AAX32597
c 24	68	3.1	1428	21 AAA99466
c 25	68	3.1	4371	21 AAA99469
26	66	3.0	8305	24 ABL33569
27	64.6	2.9	13326	24 ABL33712
28	64.4	2.9	6901	15 AAQ73703
c 29	62	2.8	17953	24 AAD38802
c 30	61.8	2.8	1591	18 AAT93780
31	61.4	2.8	5989	24 ABL54319
32	61.4	2.8	9810	24 ABL32427
33	61.2	2.8	50000	24 ABL55644
34	60.8	2.8	12120	24 AAS96695
c 35	60.6	2.8	2699	22 AAH27620
c 36	60.6	2.8	2784	22 AAH27619
c 37	60.6	2.8	4077	22 AAH27621
c 38	60.4	2.7	32392	24 ABL56203
39	60.2	2.7	21313	22 AAK82710
c 40	60.2	2.7	222930	24 ABK84349
c 41	60	2.7	17183	24 ABL32486
c 42	60	2.7	18598	24 ABL32387
c 43	59.8	2.7	4590	7 AAN60472
c 44	59.8	2.7	109906	24 ABK94411
c 45	59.6	2.7	550	19 AAV63932

ALIGNMENTS

RESULT 1
AAD38803/c
ID AAD38803 standard; DNA; 91552 BP.
XX AAD38803;
AC AAD38803;
XX
XX
DT 23-SEP-2002 (first entry)
XX
DE BAC clone K6P36 from rice variety CO39.
XX
KW Rice; chromosome 11; Indica rice cultivar; CO39; avirulence gene;
KW AVRI-CO39; rice blast pathogen; transgenic plant; plant breeding;
KW resistance; agricultural; horticultural; plant protectant; ds.
XX
XX Oryza sativa.
XX OS
XX WO200234927-A2.
XX
XX 02-MAY-2002.
XX
XX 19-OCT-2001; 2001WO-US46331.
XX
XX 20-OCT-2000; 2000US-242313P.
XX 09-JUL-2001; 2001US-303897P.
XX (WISC) WISCONSIN ALUMNI RES FOUND.
XX (USDA) US DEPT OF AGRICULTURE.
XX
XX Leong SA, Farman ML, Chauhan RS, Durfee TJ;
XX WPI; 2002-471442/50.
XX

RESULTS. 7 3

Db 65409 TTATGTATATATATATATATATTTTACATATATTCAAAAAGTTTTTAAATAAAGCAACGG 65350
QY 1021 TCAATGTGTAGTCGAAAGTCATAGTGTGTACATTAATAATACGAGGAGTATA 1076
Db 65349 TTAGTATATTTTAAAGATTCACGACGTCACAAATTTTGGGACAGAGGAGTATA 65294

RESULT 11

ABK15663/C
ID ABK15663 standard; DNA; 4569 BP.
XX
AC ABK15663;
XX
DT 21-MAY-2002 (first entry)
XX
DE Rice lipoxigenase gene 4.5kb fragment.

XX Rice; ds; lipoxigenase; RCI-1; transgenic; plant; plant antifungal;
KW rice chemically induced cDNA; promoter; transit peptide; plastid;
KW fungal mycotoxin inhibitor; plant breeding; pBSK+LOX4a.

XX Oryza sativa.

XX WO200206490-A1.

XX 24-JAN-2002.

XX 12-JUL-2001; 2001WO-EP08085.

XX 13-JUL-2000; 2000GB-0017275.

XX 15-SEP-2000; 2000GB-0022739.

XX (SYGN) SYNGENTA PARTICIPATIONS AG.

XX (UYZU-) UNIV ZUERICH.

XX Dudley R, Schaffrath, Lawton KA;

XX WPI; 2002-188550/24.

XX Novel isolated nucleic acid encoding a promoter which is capable of
PT driving chemically inducible but not wound- or pathogen-inducible
PT expression of an associated nucleotide sequence -

XX Claim 3; Page 68-69; 88pp; English.

XX The invention relates to an isolated nucleic acid molecule (a promoter of
XX rice chemically induced cDNA (RCI-1), which encodes a lipoxigenase)
XX capable of driving chemically-inducible but not wound- or pathogen-
XX inducible expression of an associated nucleotide sequence. Also
XX included are the RCI-1 cDNA, its encoded protein, a 4.5kb genomic clone
XX for the lipoxigenase gene, promoter fragments, the lipoxigenase transit
XX peptide which directs expressed proteins to the plastid, a vector
XX comprising the promoter or fragments and a transgenic plant comprising
XX the vector. The promoter or fragments are useful for expressing a
XX nucleotide sequence of interest. The transit peptide is useful for
XX targeting an associated protein of interest to plastids. A nucleic acid
XX which expresses polypeptides having lipoxigenase activity is useful for
XX inhibiting fungal mycotoxins when transformed into a plant. The
XX lipoxigenase is useful for inhibiting fungal mycotoxins. The promoter is
XX useful for regulating transcription of a chemically inducible but not
XX wound or pathogen inducible gene, which involves applying a chemical
XX regulator to a plant or seed containing a chemically regulatable
XX nucleotide sequence. Transgenic plants as described above are useful for
XX breeding improved plant lines that for example increase the effectiveness
XX of conventional methods such as herbicide or pesticide treatment or allow
XX to dispense with the methods due to their modified genetic properties.
XX New crops with improved stress tolerance can be obtained that, due to
XX their optimised genetic equipment yield harvested product of better
XX quality than products that were not able to tolerate comparable adverse
XX developmental conditions. The present sequence is the 4.5kb
XX fragment of the RCI-1 gene from plasmid pBSK+LOX4a.

XX Sequence 4569 BP; 1234 A; 1051 C; 980 G; 1304 T; 0 other;

Query Match 4.5%; Score 98.6; DB 24; Length 4569;
Best Local Similarity 61.8%; Pred. No. 2.1e-11;
Matches 175; Conservative 0; Mismatches 104; Indels 4; Gaps 1;

QY 843 TACTACCTCCCATATTTTAATGATGACGCCGCTGACCTTTTGTCCCAACGCTTTGACCATTC 902
Db 3080 TACTCTCCGCTTTTAAATAGATGACGCCGCTGACCTTTTCTCCCATCTTTTGACCATTC 3021

QY 903 GTCCTATTAAAAAATAATGATCTATTTATTTATTTATATGACTTGCATCA 962.
Db 3020 GTCCTATTAAAAAATAATGATCTATTTATTTATTTATATGACTTGCATCA 961

QY 963 AATATTTTAAAGCATGACATAAAACATTTTCATATTTTGCAAA-----AAAAAAAACGAAT 1018
Db 2960 GTCATAAAACATTCATAACAACTAAATATATATATATTTTATTAAGACGAAT 2901

QY 1019 GGTCAATGTTAGTCGAAAAGTCATGCTGTCATACATTAATAATACGAGGATATATG 1078
Db 2900 GGTCAACATGTCGAAAAAGTCACGCGCTCATCTATTAAAAACAGAGGTAGTATATC 2841

QY 1079 GGATAGCTACAGTAGCAGAGTCATGATTAAGTAGTAATGCTT 1121

Db 2840 TTATATACATCTAATCTACTAATGCTAAGCAAAAAATATTTT 2798

RESULT 12

AAD38803
ID AAD38803 standard; DNA; 91552 BP.

XX AAD38803;

XX 23-SEP-2002 (first entry)

XX BAC clone K6P36 from rice variety CO39.

XX Rice; chromosome 11; Indica rice cultivar; CO39; avirulence gene;
XX AVR1-CO39; rice blast pathogen; transgenic plant; plant breeding;
XX resistance; agricultural; horticultural; plant protectant; ds.

XX Oryza sativa.

XX WO200234927-A2.

XX 02-MAY-2002.

XX 19-OCT-2001; 2001WO-US46331.

XX 20-OCT-2000; 2000US-242313P.

XX 09-JUL-2001; 2001US-303897P.

XX (WISC) WISCONSIN ALUMNI RES FOUND.

XX (USDA) US DEPT OF AGRICULTURE.

XX Leong SA, Farman ML, Chauhan RS, Durfee TJ;

XX WPI; 2002-471442/50.

XX New PiCO39(t) polynucleotides from chromosome 11 of Indica rice
XX cultivar CO39 useful for conferring or improving resistance of plants
XX to strains of Magnaporthe grisea or other plant pathogens with
XX avirulence gene AVR1-CO39

XX Example 2; Page 68-110; 175pp; English.

XX The invention relates to a polynucleotide isolated from chromosome 11 of
XX Indica rice cultivar CO39, flanked by marker R2316 and RG1094 comprising
XX one or more genes that confer resistance to strains of Magnaporthe grisea
XX having avirulence gene AVR1-CO39. The Pi-CO39(t) polynucleotides are
XX useful for conferring or improving resistance of plants to strains of the
XX rice blast pathogen, Magnaporthe grisea and other pathogens. The
XX Pi-CO39(t) nucleic acids may be used as probes to detect the presence of
XX and/or expression of Pi-CO39(t) genes, and to produce large quantities of

CC pure Pi-C039(t) proteins. Purified gene products of Pi-C039(t) are useful
 CC in producing polyclonal or monoclonal antibodies useful as sensitive
 CC detection reagents for the presence and accumulation of Pi-C039(t)
 CC polypeptides. The transgenic plants are useful for plant breeding or
 CC directly in agricultural or horticultural applications. The present
 CC sequence is BAC clone K6P36 from rice variety CO39.

XX Sequence 91552 BP; 26676 A; 19760 C; 17854 G; 27262 T; 0 other;

Query Match 4.5%; Score 98.2; DB 24; Length 91552;
 Best Local Similarity 65.6%; Pred. No. 9.8e-11;
 Matches 162; Conservative 0; Mismatches 78; Indels 7; Gaps 1;

QY 836 TACTATTACTACCTCCATATTTTAAAGTATGACGCGCTTCACTTTTGCACAACTTGG 895

DB 33565 TAGTAAGTATCCCTCCGATTTTAAAGTATGACGCGCTTCACTTTTGCACAACTTGG 33624

QY 896 ACCATTGCTGTTATTAATAAAATATGATATCTATTTATTTATTTATGACTTGAATTC 955

DB 33625 ACCATTGCTGTTATTCABAATTTTGGCAATATAAATAATTAATGATGCTTAAAG 33684

QY 956 GTCATCAATATTTTAAAGCATGACATTAACATTTTTCATATTTGCAAAAA-----AA 1008

DB 33685 AATATTGATGACGAATCAAGTCATATAAATAAATAAATGATGATTAATTTTGTAA 33744

QY 1009 AAAACGAATGTCGAATGTTAGTGAAGTCAATGGTGTGCATACATTAATAACGGAG 1068

DB 33745 TAGACGAATGTCGAATGTTAGTGAAGTCAATGGTGTGCATACATTAATAACAGAG 33804

QY 1069 GGATAT 1075

DB 33805 GGATAT 33811

RESULT 13

ID AAC48763

AC AAC48763 standard; DNA; 694 BP.

XX AAC48763;

XX 18-OCT-2000 (first entry)

XX Arabidopsis thaliana DNA fragment SEQ ID NO: 58679.

XX Hybridisation assay; genetic mapping; gene expression control;

XX protein identification; signal transduction pathway;

XX metabolic pathway; promoter; termination sequence; ss.

XX Arabidopsis thaliana.

XX EF1033405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.

XX 05-MAR-1999; 99US-0123180.

XX 09-MAR-1999; 99US-0123548.

XX 23-MAR-1999; 99US-0125788.

XX 25-MAR-1999; 99US-0126264.

XX 29-MAR-1999; 99US-0126785.

XX 01-APR-1999; 99US-0127462.

XX 06-APR-1999; 99US-0128234.

XX 18-APR-1999; 99US-0128714.

XX 16-APR-1999; 99US-0129845.

XX 19-APR-1999; 99US-0130077.

XX 21-APR-1999; 99US-0130449.

XX 23-APR-1999; 99US-0130510.

XX 28-APR-1999; 99US-0130891.

XX 30-APR-1999; 99US-0131449.

XX 30-APR-1999; 99US-0132048.

XX 30-APR-1999; 99US-0132407.

PR 04-MAY-1999; 99US-0132484.

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PR 06-MAY-1999; 99US-0132486.

PR 07-MAY-1999; 99US-0132487.

PR 11-MAY-1999; 99US-0132863.

PR 14-MAY-1999; 99US-0134256.

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PR 20-MAY-1999; 99US-0134941.

PR 21-MAY-1999; 99US-0135124.

PR 21-MAY-1999; 99US-0135353.

PR 24-MAY-1999; 99US-0135629.

PR 25-MAY-1999; 99US-0136021.

PR 27-MAY-1999; 99US-0136392.

PR 28-MAY-1999; 99US-0136782.

PR 01-JUN-1999; 99US-0137222.

PR 03-JUN-1999; 99US-0137528.

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PR 07-JUN-1999; 99US-0137724.

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PR 18-JUN-1999; 99US-0139463.

PR 18-JUN-1999; 99US-0139750.

PR 18-JUN-1999; 99US-0139763.

PR 21-JUN-1999; 99US-0139817.

PR 22-JUN-1999; 99US-0139899.

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PR 24-JUN-1999; 99US-0140695.

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PR 29-JUN-1999; 99US-0140991.

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PR 01-JUL-1999; 99US-0141842.

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PR 09-JUL-1999; 99US-0142920.

PR 12-JUL-1999; 99US-0142977.

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PR 15-JUL-1999; 99US-0144005.

PR 16-JUL-1999; 99US-0144085.

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PR 19-JUL-1999; 99US-0144325.

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PR 19-JUL-1999; 99US-0144335.

PR 20-JUL-1999; 99US-0144352.

PR 20-JUL-1999; 99US-0144632.

PR 20-JUL-1999; 99US-0144884.

PR 21-JUL-1999; 99US-0144814.

PR 21-JUL-1999; 99US-0145086.

PR 21-JUL-1999; 99US-0145088.

RESULT 14	
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ID	AAC44265 standard; DNA; 695 BP.
XX	
AC	AAC44265;
XX	
DI	18-OCT-2000 (first entry)
XX	
DE	Arabidopsis thaliana DNA fragment SEQ ID NO: 42224.
XX	
KW	Hybridisation assay; genetic mapping; gene expression control;
KW	protein identification; signal transduction pathway;
KW	metabolic pathway; promoter; termination sequence; ss.
XX	
OS	Arabidopsis thaliana.
XX	
PN	EPI033405-A2.
XX	
PD	06-SEP-2000.
XX	
PF	25-FEB-2000; 2000EP-0301439.
XX	
PR	25-FEB-1999; 99US-0121825.
PR	05-MAR-1999; 99US-0123180.
PR	09-MAR-1999; 99US-0123548.
PR	23-MAR-1999; 99US-0125788.
PR	25-MAR-1999; 99US-0126264.
PR	29-MAR-1999; 99US-0126785.
PR	01-APR-1999; 99US-0127462.
PR	06-APR-1999; 99US-0128234.
PR	08-APR-1999; 99US-0128714.
PR	16-APR-1999; 99US-0129845.
PR	19-APR-1999; 99US-0130077.
PR	21-APR-1999; 99US-0130449.

PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
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PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
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PR 05-AUG-1999; 99US-0147192.
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PR 06-AUG-1999; 99US-0147416.
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PR 20-SEP-1999; 99US-0154779.
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PR 24-SEP-1999; 99US-0155659.
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PR 05-OCT-1999; 99US-0157753.
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PR 13-OCT-1999; 99US-0159293.
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PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.

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PR 14-OCT-1999; 99US-0159637.
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PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 23-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 4.3%; Score 95.4; DB 21; Length 695;
Best Local Similarity 67.2%; Pred. No. 4.6e-11;
Matches 133; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

QY 1693 TGTGATGCGAGTGTGCGCACCAGGTTGTCGAGATGCCCGCGTGTGCGTGGAGGAGG 1752
Db 240 TGATCAAGGAGATTGTCGTACCAAGACTTTCGAGATGCCACCATGACTGTCGTGAGG 299

QY 1753 CGATGGGACGCTAGTGAATGTGGACCAACTTCTACGCTTCAGAGAGAGAGACCG 1812
Db 300 CAGTCGACGCTGGAACACTGACGTCACGACTTCTATGCTTCCAAAATGAAGAACTG 359

QY 1813 GGGAGATGAAGCTCCTGTACAGAGAGAGAGAGGAGGCTTCGCTCTCATCGTCCCAAGG 1872
Db 360 GTGAGATGAACATAGTGTACAGAGAGAGAGAGAGGAGGTTACGCTCTCATATCCCAAGA 419

QY 1873 GAGACGGTCAFTCTCCAAAGG 1893
Db 420 AAGACGGGAGGCGCGAAGG 440

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```

RESULT 15
AAT93780
ID AAT93780 standard; DNA; 1591 BP.
XX AC AAT93780;
XX DT 13-FEB-1998 (first entry)
XX DE Oryza sativa pathogen inducible regulatory element Pr-10c cDNA.
XX KW Pathogen inducible regulatory element; MAG-7; Magnaporthe grisea;
XX KW promoter region; gene induction; pathogen-inducible regulatory element;
XX KW Co39 rice seedling genomic library; disease resistance; rice; ds.
XX OS Oryza sativa.
XX PN US5677175-A.
XX PD 14-OCT-1997.
XX PF 11-OCT-1996; 96US-0005362.
XX PR 13-OCT-1995; 95US-0005362.
XX PA (PURD ) PURDUE RES FOUND.
XX PI Hodges TK, McGee JD;
XX WPI; 1997-511872/47.

```

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XX Plant expression vector with pathogen-inducible regulatory element -
PT used for increasing disease resistance of plants
XX Claim 1; Columns 11-14; 8pp; English.
XX CC The present sequence, Pr-10c, is a pathogen inducible regulatory
CC element. It was identified by screening a Co39 rice seedling genomic
CC library with a cDNA clone, MAG-7, of a gene whose transcripts appeared in
CC Co39 rice seedlings 72 hours after inoculation with Magnaporthe grisea.
CC Induced expression of the Pr-10c gene was not detected after infection
CC with M. grisea throughout a 144 hour time period. The Pr-10c sequence is
CC used to make a novel plant expression vector comprising a
CC pathogen-inducible regulatory element and a core promoter, where the
CC regulatory element is selected from three rice genomic DNA sequences
CC AAT93778-80. The vectors are used for increasing the disease resistance
CC of plants.
XX SQ Sequence 1591 BP; 464 A; 289 C; 373 G; 465 T; 0 other;

Query Match 4.2%; Score 91.4; DB 18; Length 1591;
Best Local Similarity 66.9%; Pred. No. 5e-10;
Matches 164; Conservative 0; Mismatches 71; Indels 10; Gaps 2;

QY 841 ATTACTACCTCCATATTTTAATGATGAGCGCGCTCACTTTTGT---CCACGTTGAC 897
Db 723 AATACTCCTCCGTTTCAAAATGTTGACCCGCTGATTTTTTTTGTATATGTTGAT 782

QY 898 CATTGCTTATTAATAAAAAAATAATGATCTATCTATTATTATTATTATGACUTGATTCGT 957
Db 783 CATTGCTTATTAATAATAATAATGATCTATCTATTATTATTATTATTCGATGACTGAT 842

QY 958 CATCAAAATATTTTAAAGCATGACATAAACAATTTTCATATTTTGCAGAAA-----AAAAA 1010
Db 843 TCTTAATAATATCTTTCATGTCGACATATAGTTTACATATTTTACAAATTTTGTGATA 902

QY 1011 AAACGAGTGTCAAACTGTAGTCGAAAACCTCAATGGTGTATCATATTAATAACGAGGG 1070
Db 903 AGACGAGGTCGCAACATGTGCTAAAAAATTAAGGTCATATATTTTGAACGAGGG 962

QY 1071 ATTAT 1075
Db 963 AGTAT 967

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Search completed: March 26, 2003, 05:14:07
Job time : 777.159 secs

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 25, 2003, 19:50:00 ; Search time 2242.74 Seconds
(without alignments)
15894.084 Million cell updates/sec

Title: US-09-702-134-7212_COPY_10200_12400

Perfect score: 2201
Sequence: 1 cgccttgctgttgcgcgc.....tagcttgctgttgcgtga 2201

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

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EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vit:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	582.6	26.5	714	17 AQ051086	AQ051086 nbx00005a
2	559.6	25.4	653	13 BI305800	BI305800 NL1_M15
3	529	24.0	638	14 BQ908458	BQ908458 T008E03 O
4	491.4	22.3	597	9 AU094078	AU094078 AU094078
5	449	20.4	570	9 AU056564	AU056564 AU056564
6	445.6	20.2	575	13 BI810180	BI810180 J001B06 O

7	443	20.1	522	13	BM420118	BM420118 R023H11 O
8	432	19.6	534	13	BM420133	BM420133 R024B06 O
9	429.4	19.5	525	14	BQ908495	BQ908495 T008H05 O
10	418.6	19.0	460	10	BE230575	BE230575 99AS79 R1
11	416.8	18.9	627	13	BM037750	BM037750 S098C08 S
12	414.4	18.8	443	14	BQ908635	BQ908635 T012B09 O
13	410.0	18.6	516	13	BI811299	BI811299 N001C12 O
14	398.8	18.1	539	13	BM038608	BM038608 V006C02 O
15	397.4	18.1	531	14	BQ906047	BQ906047 L010D02 O
16	395	17.9	581	13	BI810545	BI810545 K001B04 O
17	389.4	17.7	576	13	BI811225	BI811225 M001F09 O
18	387	17.6	509	13	BM038731	BM038731 V009A06 O
19	382.4	17.4	515	13	BM421616	BM421616 V017G11 O
20	378.6	17.2	483	13	BI810402	BI810402 J007A12 O
21	377.6	17.2	598	14	BQ907480	BQ907480 P007B02 O
22	368	16.7	437	14	C72803	C72803 C72803 Rice
23	362	16.4	399	13	BI806502	BI806502 S067D01 S
24	361.2	16.4	603	10	BE229715	BE229715 98SN0103
25	360.8	16.4	404	14	BQ280726	BQ280726 WHE3004.B
26	352.6	16.0	557	13	BM038147	BM038147 U003E10 O
27	341.6	15.5	514	13	BM039048	BM039048 V013F10 O
28	341	15.5	521	13	BM420069	BM420069 R023B08 O
29	330.4	15.0	540	9	AU056563	AU056563 AU056563
30	328.4	14.9	549	14	BQ908614	BQ908614 T011G07 O
31	313.4	14.2	490	13	BM419787	BM419787 R018G06 O
32	313	14.2	552	13	BI811322	BI811322 N001G10 O
33	308	14.0	325	9	AU056562	AU056562 AU056562
34	301.6	13.7	604	13	BM038823	BM038823 V010C06 O
35	280.2	12.7	397	14	BQ908902	BQ908902 T016H08 O
36	278.8	12.7	540	13	BI807063	BI807063 S082B05 S
37	253.6	11.5	466	14	BQ908540	BQ908540 T010B09 O
38	248	11.3	513	13	BI810148	BI810148 I005F07 O
39	236.2	10.7	752	12	BF265998	BF265998 HV_Cra001
40	233.6	10.6	858	12	BF262651	BF262651 HV_Cra000
41	231.6	10.5	568	13	BQ468880	BQ468880 BJ468880
42	230.8	10.5	595	13	BI679710	BI679710 949078B06
43	228.2	10.4	757	12	BF627121	BF627121 HVSME000
44	216.6	9.8	852	12	BF629402	BF629402 HVSME001
45	214.8	9.8	380	13	BM421344	BM421344 V008A01 O

ALIGNMENTS

RESULT 1
AQ051086 714 bp DNA linear GSS 24-MAR-1999
LOCUS nbx00005aC11r CUGI Rice BAC Library Oryza sativa genomic clone
DEFINITION nbx00005E21r, DNA sequence.
ACCESSION AQ051086
VERSION AQ051086.2 GI:4501804
KEYWORDS GSS.
SOURCE Oryza sativa.
ORGANISM Oryza sativa.
REFERENCE 1 (bases 1 to 714)
AUTHORS Wing, R.A. and Dean, R.A.
TITLE A BAC End Sequencing Framework to Sequence the Rice Genome
JOURNAL Unpublished (1999)
COMMENT On Mar 23, 1999 this sequence version replaced gi:3325391.
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: GGAAACAGCTATGACCATG
Class: BAC ends
High quality sequence start: 31
High quality sequence stop: 250.

Phylogeny: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Eriophytaceae; Oryzaceae; Oryza.


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        /organism="Oryza sativa"
        /strain="Japonica"
        /cultivar="Nipponbare"
        /db_xref="taxon:4530"
        /clone="mbx0005E2ir"
        /clone_lib="CUGR Rice BAC Library"
        /tissue_type="Leaf"
        /lab_host="E. coli DH10B"
        /note="Vector: pBelobAC11; Site1: HindIII; Site2: HindIII; Rice is one of two most popular grains in the world. Half of the world population especially those inhabiting highly populated areas of the humid tropics and subtropics, rely on rice as their primary source of carbohydrate. Monocotyledonous rice is a diploid plant (2n=24) with a haploid genome equivalent of 431 Mbp (Arumuganathan and Earle, 1991). The relatively small genome of rice, three times larger than that of Arabidopsis, makes it suitable for genomic studies. In order to facilitate positional cloning, physical mapping and genome sequencing of rice, we have constructed a BAC library from Oryza sativa, Nipponbare variety. The library contains 36,864 clones with an average insert size of 128.5 kb providing 10.9 haploid genome equivalents. The deep coverage allows the isolation a particular sequence with a probability of 99.9 %. Two high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening."
      BASE COUNT      174 a 207 c 137 g 196 t
      ORIGIN
        Query Match      26.5%; Score 582.6; DB 17; Length 714;
        Best Local Similarity 93.0%; Pred. No. 7.3e-109;
        Matches 654; Conservative 0; Mismatches 44; Indels 5; Gaps 4;

QY 67 CTCCTCTCTCTGTATTAGACAGCAACAGTAGCTAGCGAGCGAGCTGCGAGA 126
Db 1 CTCCTCTCTCTGTATTAGACAGCAACAGTAGCTAGCGAGCGAGCTGCGAGA 60
QY 127 GCAGAGCATGTTCTTCTCTAGCTATTAGTGTGGGGAATAAGTGGTCCGCCACCA 186
Db 61 GCAGAGCATGTTCTTCTCTAGCTATTAGTGTGGGGAATAAGTGGTCCGCCACCA 120
QY 187 CGCAGCAATGCGCCTCGCGCGCCCTCTTCCATCACCATCACCATCACCATGTCACAGC 246
Db 121 CGCAGCAATGCGCCTCGCGCGCCCTCTTCCATCACCATCACCATCACCATGTCACAGC 180
QY 247 AGCTGAGCTCCCTCGCTCTCTCGTCTCGTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCT 306
Db 181 AGCTGAGCTCCCTCGCTCTCTCGTCTCGTCCGCTCCGCTCCGCTCCGCTCCGCTCCGCT 240
QY 307 GGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 366
Db 241 GGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
QY 367 GCGCGTGTCCGCTGCGGATGCTGCGGAGCGGCGCCCTCTCCCTCGGTCGCGCTCATATAG- 425
Db 301 GCGCGTGTCCGCTGCGGATGCTGCGGAGCGGCGCCCTCTCCCTCGGTCGCGCTCATATAGC 360
QY 426 CAGGCGCCAGCAAGTCAGGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 485
Db 361 CAGGCGCCAGCAAGTCAGGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 420
QY 486 TTTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 545
Db 421 TTTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 478
QY 546 ATGATTAATTTCTAGATTCATATATATATATATATATATATATATATATATATATATATAT 605
Db 479 ATGATTAATTTCTAGATTCATATATATATATATATATATATATATATATATATATATATAT 538
QY 606 TAACCTGAAACAGAGGGAGTATATATAAATCGGTAATGGATACAGATATTTCTTTTAT 665

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Db 539 TAACCCGAACAGAGGGAGTATATCTAATTCGTAAATGGAATACAGATTGCACTCAAT 598
QY 666 AATTGAGCCTTTTAAATAGTACTAGTAATTCACGAACTACAGAT-TCCTCTTTATTGGT 724
Db 599 AATTGAGCCTTTTAAATAGTACTAGTAATTCACGAACTACAGATTCATCTCAATTGG 658
QY 725 TATATT-AGTAGTAATTTGGTCTCAGTACAGTAATTTCTATTTATATAC 766
Db 659 TATATTGAGTGGGAATCGCTGACCTTAGACATCTATCTCTAC 701

RESULT 2
BI305800/c 653 bp mRNA linear EST 20-JUL-2001
LOCUS NL_1_M15 Drought stress (leaf) Oryza sativa cDNA clone NL_1_M15 3',
DEFINITION mRNA sequence.
ACCESSION BI305800
VERSION BI305800.1 GI:14981109
KEYWORDS EST.
SOURCE Oryza sativa.
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 653)
AUTHORS Reddy A.R., Ramakrishna W., Chandrasekhar A., Nagabhushan, I.,
Ravindrababu, P. and Bennetzen, J.L.
Novel EST enrichment with normalized cDNA libraries from drought
stressed rice (Oryza sativa L.cv Nagina 22)
Unpublished (2001)
CONTACT: Reddy AR
DEPARTMENT of Plant Sciences, School of Life Sciences
University of Hyderabad
P.O. Central University, Hyderabad-500 046, A.P., India
Tel: 0091-40-3010265
Fax: 0091-40-3010145
Email: arjuls@uohyd.ernet.in
Insert Length: 653 Std Error: 0.00
Plate: 1 row: M column: 15
Seq primer: GTAAACGAGCGCCAGTG.
FEATURES
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        /cultivar="Nagina 22 (indica sub sp)"
        /db_xref="taxon:4530"
        /clone="NL_1_M15"
        /clone_lib="Drought stress (leaf)"
        /tissue_type="Entire leaf tissue"
        /dev_stage="35 day-old seedlings"
        /note="Organ: Leaf; Vector: p7T3Pac; ESTs from normalized
leaf cDNA Library from drought stressed seedlings "
      BASE COUNT      144 a 159 c 187 g 162 t
      ORIGIN
        Query Match      25.4%; Score 559.6; DB 13; Length 653;
        Best Local Similarity 88.9%; Pred. No. 3.7e-104;
        Matches 648; Conservative 0; Mismatches 5; Indels 76; Gaps 1;

QY 1413 AGCCAGCATGCTCGCTCCCTCCATCATCAAGAGCAAGCTCCAGGATCAAGGAGA 1472
Db 653 AGCCAGCATGCTCGCTCCCTCCATCATCAAGAGCAAGCTCCAGGATCAAGGAGA 594
QY 1473 AGGAGACGAGCTCGGCACTCAAGGGAGCAAGCCCGCTCTCCGACTGGCGCCCAT 1532
Db 593 AGGAGACGAGCTCGGCACTCAAGGGAGCAAGCCCGCTCTCCGACTGGCGCCCAT 534
QY 1533 CATTCGTCGACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1592
Db 533 CATTCGTCGACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 474
QY 1593 TCGGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1652

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Db 473 TCGCGCGCGGAGGACGAGGACACGGTGTCTACCA----- 441
QY 1653 GCATATTAATCAATCATTCATGACCAATTAATGCAACTGTGAATCAGGTGGTGGCG 1712
Db 440 -----AGGTGGTGGCG 430
QY 1713 ACCAAGGTGTTGAGATGCGCGCGTGTGCGTGGAGAGGCGATGGAGCACTAGTGAAT 1772
Db 429 ACCAAGGTGTTGAGATGCGCGCGTGTGCGTGGAGAGGCGATGGAGCACTAGTGAAT 370
QY 1773 GTGGACCAACACTTTCACGCTTCAGAGACGAGAGACCGGGAGATGAAGCTCTGTAC 1832
Db 369 GTGGACCAACACTTTCACGCTTCAGAGACGAGAGACCGGGAGATGAAGCTCTGTAC 310
QY 1833 AAGAGGAGGAGAGGCTTGGCTCTCATGTCCTCCCAAGGAGAGCGGTCACTCCACAAG 1892
Db 309 AAGAGGAGGAGAGGCTTGGCTCTCATGTCCTCCCAAGGAGAGCGGTCACTCCACAAG 250
QY 1893 GAGACCATCCCAACTCTGACCAACACACCCCTGCTGCTGCTAGCCCTCTACACCTC 1952
Db 249 GAGACCATCCCAACTCTGACCAACACACCCCTGCTGCTGCTAGCCCTCTACACCTC 190
QY 1953 CTGCAACCACTCTCTATTTCTATTTCTATTTCTATTTCTATTTCTATTTCTATTTCT 2012
Db 189 CTGCAACCACTCTCTATTTCTATTTCTATTTCTATTTCTATTTCTATTTCTATTTCT 130
QY 2013 ACTAGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2072
Db 129 ACTAGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 70
QY 2073 ATCGATCGACTCTTGACTCTGTTTAAACCAACTGTTTTCATATTAATTAATTAAT 2132
Db 69 ATCGATCGACTCTTGACTCTGTTTAAACCAACTGTTTTCATATTAATTAATTAATTA 10
QY 2133 TGATTTTTC 2141
Db 9 TGATTTTTC 1

RESULT 3
BO908458
LOCUS BO908458 638 bp mRNA linear EST 19-AUG-2002
DEFINITION T008503 Oryza sativa mature leaf library induced by M.grisea Oryza
sativa cDNA clone T008E03, mRNA sequence.
ACCESSION BO908458
VERSION BO908458.1 GI:22307236
KEYWORDS EST.
SOURCE Oryza sativa.
ORGANISM Oryza sativa

REFERENCE
AUTHORS Dong,H.T., Li,D.B., Zhuang,X.F., Dai,C.G., Sun,L.X., Pei,Y.X., Wu
,H.F., Jiang,Y.X., Yu,F.C., Gao,Q.K. and Lou,Y.C.
TITLE A Gene Expression Screen in Oryza sativa
JOURNAL Unpublished (2001)
COMMENT Contact: Dong HT
Laboratory of Functional Genetics
Bio-Technology Institute of Zhejiang University
Kaixuan Road 268, Hangzhou, Zhejiang, P.R.China
Tel: 0086-571-86892051
Fax: 0086-571-86961525
Email: htdong@zjuem.zju.edu.cn
Seq primer: M13 forward primer.
FEATURES
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location/Qualifiers
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/clone="T008E03"
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M.grisea"
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/Note="Vector: pSport2"
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Best Local Similarity 89.08; Pred. No. 6.7e-98;
Matches 615; Conservative 0; Mismatches 0; Indels 76; Gaps 1;
QY 1365 CCAGGCGCCACCGCGCTCATCCGCGCGAGGAGGAGCGCCAGTCCACCTAGCCAGCATCG 1424
Db 4 CCAAGCGCCACCGCGCTCATCCGCGCGAGGAGGAGCGCGAGTCCACCTAGCCAGCATCG 63
QY 1425 ACCTCGCTCTCTCCATCATCAAGAGGAGAGCTCAGAGAGATCAGAGAGAGGAGACCGAG 1484
Db 64 ACCTCGCTCTCTCCATCATCAAGAGGAGAGCTCAGAGAGATCAGAGAGAGGAGACCGAG 123
QY 1485 TCGCCACCTCTAAGGGGACCAAGCCCGCTCTCCGACTGGCGCCATCATTTGCTGCACA 1544
Db 124 TCGCCACCTCTAAGGGGACCAAGCCCGCTCTCCGACTGGCGCCATCATTTGCTGCACA 183
QY 1545 ACAACGACGACGACGCGCCAGCCCGAGCTCAAGGATCTGGAGAGGCGCGCGCGAGG 1604
Db 184 ACAACGACGACGACGCGCCAGCCCGAGCTCAAGGATCTGGAGAGGCGCGCGCGAGG 243
QY 1605 ACAGGACACGGTGTCTCACCAGGCTCTGCAGTCTGCATGATCATCAATGCATATAATCA 1664
Db 244 ACAGGACACGGTGTCTCACCAGGCTCTGCAGTCTGCATGATCATCAATGCATATAATCA 264
QY 1665 AATCATTCATGAACCAAAATTAATGCAACTGTGAATGCAAGTGTGGCGCACCAAGGTGTC 1724
Db 265 -----AGGTGGTGGCGCACCAAGGTGTC 287
QY 1725 GAGATGCGCGCGCTGTGCGTGGAGAGGCGATGGAGCAGCTAGTGAATGTGGACCAAC 1784
Db 288 GAGATGCGCGCGCTGTGCGTGGAGAGGCGATGGAGCAGCTAGTGAATGTGGACCAAC 347
QY 1785 TTCTACGCTCTCAGAGACGAGAGACCGGGAGATGAACGCTCTGTACAGAGAGAGGAA 1844
Db 348 TTCTACGCTCTCAGAGACGAGAGACCGGGAGATGAACGCTCTGTACAGAGAGAGGAA 407
QY 1845 GGAGGCTGGGTCTCATCTGCTCCCAAGGAGAGCGTCAATCCCAAGGAGACCATCCCC 1904
Db 408 GGAGGCTGGGTCTCATCTGCTCCCAAGGAGAGCGTCAATCCCAAGGAGACCATCCCC 467
QY 1905 AACTCTGACCAACCAACCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1964
Db 468 AACTCTGACCAACCAACCCCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 527
QY 1965 CCTCATTTGCTAATTAATTTCTATGCTTGGCCCAAGAGTCTCTAATTAATTAATTAAT 2024
Db 528 CCTCATTTGCTAATTAATTTCTATGCTTGGCCCAAGAGTCTCTAATTAATTAATTAAT 587
QY 2025 TAATCCAAAGTGATGAGAGAGGCTCTTTGATTT 2055
Db 588 TAATCCAAAGTGATGAGAGAGGCTCTTTGATTT 618

RESULT 4
BO9094078
LOCUS BO9094078 597 bp mRNA linear EST 03-APR-2002
DEFINITION A0094078 Rice panicle at flowering stage Oryza sativa (japonica
cultivar-group) cDNA clone E2287, mRNA sequence.
ACCESSION A0094078
VERSION A0094078.1 GI:8856760
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group).
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 597)
REFERENCE
AUTHORS Sasaki,T. and Yamamoto,K.
```

TITLE Rice cDNA from panicle at flowering stage (2000)
 JOURNAL Unpublished (2000)
 COMMENT Contact: Takuji Sasaki
 National Institute of Agrobiological Resources
 Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
 305-8602, Japan
 Tel: 81-298-38-7441
 Fax: 81-298-38-7468
 Email: tsasaki@abr.affrc.go.jp, URL: http://rgp.dna.affrc.go.jp/
 PROJECT = "RGP".

FEATURES
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 /clone="E2287"
 /clone_lib="Rice panicle at flowering stage"
 /dev_stage="flowering stage"
 /note="Organ: panicle; Rice cDNA from panicle at flowering stage"

BASE COUNT 156 a 159 c 138 g 140 t 4 others
 ORIGIN

Query Match 22.3%; Score 491.4; DB 9; Length 597;
 Best Local Similarity 87.7%; Pred. No. 3.3e-90;
 Matches 578; Conservative 0; Mismatches 5; Indels 76; Gaps 1;

QY 1494 TCAAGGGGACCAAGCCCGCTCCGACTGCGCGCCGCATATCTCTGACCAACAGGAGC 1553
 Db 1 TCAAGGGGACCAAGCCCGCTCCGACTGCGCGCCGCATATCTCTGACCAACAGGAGC 60

QY 1554 ACAGCCGCCAGCCAGCTCAAGATCTGAGAGAGCGCTCGCGCCGAGGAGGAGACA 1613
 Db 61 ACAGCCGCCAGCCAGCTCAAGATCTGAGAGAGCGCTCGCGCCGAGGAGGAGACA 120

QY 1614 CGGTGCTCACCAGTCTGCGAGTCTGATGATCATGATGATATTAATCAATCATCA 1673
 Db 121 CGGTGCTCACC----- 132

QY 1674 TGAACCAAAATTAATGCAATGTGAATGCGAGTGGTGCACCAAGGTGTCGAGATGCG 1733
 Db 133 -----AGGTGGTGCACCAAGGTGTCGAGATGCG 164

QY 1734 CCCTGTGCGTGGAGGAGGAGGAGTGAATGATGATGATGATGATGATGATGATGATG 1793
 Db 165 CCCTGTGCGTGGAGGAGGAGGAGTGAATGATGATGATGATGATGATGATGATGATG 224

QY 1794 TTCAGAGACGAGACACCGGGAGATGAAGTCTCTGACAGAGAGGAGGAGGAGGCTTC 1853
 Db 225 TTCAGAGACGAGACACCGGGAGATGAAGTCTCTGACAGAGAGGAGGAGGAGGCTTC 284

QY 1854 GTCTCATGCTCCCAAGGAGGAGTCACTCTCCACAGGAGACCATCCCAACTCTGAC 1913
 Db 285 GTCTCATGCTCCCAAGGAGGAGTCACTCTCCACAGGAGACCATCCCAACTCTGAC 344

QY 1914 CACACACCCCTCCCTGCTGCTAGCTCTGATGATGATGATGATGATGATGATGATG 1973
 Db 345 CACACACCCCTCCCTGCTGCTAGCTCTGATGATGATGATGATGATGATGATGATG 404

QY 1974 CTAAATATTTCTATGCTTCCCAAGAGTCTCTAAATATTAATTAATTAATTAATTAAT 2033
 Db 405 CTAAATATTTCTATGCTTCCCAAGAGTCTCTAAATATTAATTAATTAATTAATTAAT 464

QY 2034 TGATGAGAGAGTCTTGTATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2093
 Db 465 TGATGAGAGAGTCTTGTATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 524

QY 2094 CTGTTAAACCACTGTTTTCATATTAATTAATTAATTAATTAATTAATTAATTAATTA 2152
 Db 525 CTGTTAAACCACTGTTTTCATATTAATTAATTAATTAATTAATTAATTAATTAATTA 583

RESULT 5

AU056564 570 bp mRNA linear EST 01-APR-2002
 LOCUS AU056564 Oryza sativa mature leaf Nipponbare Oryza sativa (japonica
 DEFINITION cultivar-group) cDNA clone S20686_22, mRNA sequence.
 ACCESSION AU056564
 VERSION AU056564.1 GI:4715447
 KEYWORDS EST.
 SOURCE Oryza sativa (japonica cultivar-group).
 ORGANISM Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 REFERENCE 1 (bases 1 to 570)
 AUTHORS Yamamoto, K. and Sasaki, T.
 TITLE Rice cDNA from mature leaf
 JOURNAL Unpublished (1999)
 COMMENT Contact: Takuji Sasaki
 National Institute of Agrobiological Resources
 Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
 305-8602, Japan
 Tel: 81-298-38-7441
 Fax: 81-298-38-7468
 Email: tsasaki@abr.affrc.go.jp, URL: http://rgp.dna.affrc.go.jp/
 PROJECT = "RGP".

FEATURES
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 /organism="Oryza sativa (japonica cultivar-group)"
 /cultivar="Nipponbare"
 /db_xref="taxon:39947"
 /clone="S20686_22"
 /clone_lib="Oryza sativa mature leaf Nipponbare"
 /tissue_type="mature leaf"
 BASE COUNT 148 a 153 c 125 g 137 t 7 others
 ORIGIN

Query Match 20.4%; Score 449; DB 9; Length 570;
 Best Local Similarity 98.7%; Pred. No. 1.6e-81;
 Matches 449; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1702 AGTGTGTCGCGACCAAGGTGTGAGATGCGCGCTGCTGCGTGGAGGAGCGATGGAGC 1761
 Db 100 AGTGTGTCGCGACCAAGGTGTGAGATGCGCGCTGCTGCGTGGAGGAGCGATGGAGC 159

QY 1762 AGTGTGTCGCGACCAAGGTGTGAGATGCGCGCTGCTGCGTGGAGGAGCGATGGAGC 1821
 Db 160 AGTGTGTCGCGACCAAGGTGTGAGATGCGCGCTGCTGCGTGGAGGAGCGATGGAGC 219

QY 1822 ACCTCTGTGACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1881
 Db 220 ACCTCTGTGACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 279

QY 1882 ATCTCACAAGGAGAGCACCACCCCAACTCTGACCCACCCACCCACCCACCCACCC 1941
 Db 280 ATCTCACAAGGAGAGCACCACCCCAACTCTGACCCACCCACCCACCCACCCACCC 339

QY 1942 CTCTACACCTCTGACACCACTCTGACCTCTGACCTCTGACCTCTGACCTCTGACCT 2001
 Db 340 CTCTACACCTCTGACACCACTCTGACCTCTGACCTCTGACCTCTGACCTCTGACCT 399

QY 2002 CTCTAAATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2061
 Db 400 CTCTAAATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 459

QY 2062 CGTGTACATCGATCGATCGATCGATCGATCGATCGATCGATCGATCGATCGATCGAT 2121
 Db 460 CGTGTACATCGATCGATCGATCGATCGATCGATCGATCGATCGATCGATCGATCGAT 519

QY 2122 TATATTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2156
 Db 520 TATATTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 554

RESULT 6

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B1810180
LOCUS      B1810180          575 bp      mRNA      linear      EST 02-OCT-2001
DEFINITION J001B06 Oryza sativa mature leaf library induced by M.grisea Oryza
            sativa cDNA clone J001B06, mRNA sequence.
ACCESSION  B1810180
VERSION    B1810180.1 GI:15857368
KEYWORDS   EST.
SOURCE     Oryza sativa.
            Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE  1 (bases 1 to 575)
AUTHORS   Dong,H.T., Li,D.B., Zhuang,X.F., Dai,C.G., Sun,L.X., Pei,Y.X., Wu
            ,H.F., Jiang,Y.X., Yu,F.C., Gao,Q.K. and Lou,Y.C.
TITLE     A Gene Expression Screen in Oryza sativa
JOURNAL   Unpublished (2001)
COMMENT   Contact: Dong HT
            Laboratory of Functional Genetics
            Bio-technology Institute of Zhejiang University
            Kaixuan Road 268#, Hangzhou, Zhejiang, P.R.China
            Tel: 0086-571-86892051
            Fax: 0086-571-86961525
            Email: htdong@zjuem.zju.edu.cn
            Seq primer: M13 forward primer.
            Location/Qualifiers
FEATURES   source
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             /organism="Oryza sativa"
             /db_xref="taxon:4530"
             /clone_lib="J001B06"
             /clone_lib="Oryza sativa mature leaf library induced by
             M.grisea"
             /tissue_type="leaf"
             /dev_stage="Mature stage"
             /note="Vector: pSport2"
BASE COUNT 156 a 153 c 133 g 133 t
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Query Match 20.2%; Score 445.6; DB 13; Length 575;
Best Local Similarity 93.8%; Pred. No. 7.7e-81;
Matches 540; Conservative 0; Mismatches 29; Indels 7; Gaps 7;
QY 1561 CCAGGCCACGCTCAAGATCTGGAGGAGCGCTCGCGCGGAGGACGAGGACAGGCTGTG 1620
DB 2 CCAGGCCACGCTCAAGATCTGGAGGAGCGCTCGCGCGGAGGACGAGGACAGGCTGTG 60
QY 1621 CACCAAGGTCGAGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1680
DB 61 CACCAAGGTCGAGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 120
QY 1681 AATTAATGCAACGTGTAATGCA-GGTGGTGGCACCAGCAAGGTGTCGAGATGCCCGCTG 1739
DB 121 AATTAATGCAACGTGTAATGCAAGGTGTCGAGATGCCCGCTGTCGAGATGCCCGCTG 180
QY 1740 TCGGTGGAGGAGCGATGGAGCA-GCTAGTGAATGTGGACCAACAATCTTACGCCCTTCAG 1798
DB 181 TC-GTGGAGGAGTCGATGGAGCAGCTAGTGAATGTGGACCAACAATCTTACGCCCTTCAG 239
QY 1799 AGACGAGAAGACCGGGGAGATGAAGCTCTGTACAGAGGAGGAGGAGGAGGAGGAGGAGT 1858
DB 240 AGACGAGAAGACCGGGGAGATGAAGCTCTGTACAGAGGAGGAGGAGGAGGAGGAGGAGT 299
QY 1859 CATCGTCCCAAGGAGGAGGAGTCACTCCACAGGAGACCATCCCAACTCTGACCAACCA 1918
DB 300 CATCGTCCCAAGGAGGAGGAGTCACTCCACAGGAGGAGGAGGAGGAGGAGGAGGAGT 358
QY 1919 CCACCCCTCCCTTGCTGCTAGCCTCTACACCTCTGATCAACCAATCCCAATCCCAAT 1977
DB 359 CCACCCCTCCCTTGCTGCTAGCCTCTACACCTCTGATCAACCAATCCCAATCCCAAT 418
QY 1978 TTATTTCTATGCTTGGCCAGAGTCTTAATATTTACTAGTATTAATTAATCCCAAT 2036
DB 419 TTATTTCTATGCTTGGCCAGAGTCTTAATATTTACTAGTATTAATTAATTAATCCCAAT 478
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QY 2037 TGAGAGAGGCTTTGATTTTGTCTCCGTACATCGATCGATCGATCGATCGATCGATCG 2096
DB 479 TGAGAGAGGCTTTGATTTTGTCTCCGTACATCGATCGATCGATCGATCGATCGATCG 538
QY 2097 TTTAACCACACGTTTTCGATATATTTATTTATTTAA 2132
DB 539 TTTAACCACACGTTTTCGATATATTTATTTATTTAA 574

RESULT 7
LOCUS    BM420118          522 bp      mRNA      linear      EST 28-JAN-2002
DEFINITION R023H11 Oryza sativa mature leaf library induced by M.grisea Oryza
            sativa cDNA clone R023H11, mRNA sequence.
ACCESSION  BM420118
VERSION    BM420118.1 GI:18386920
KEYWORDS   EST.
SOURCE     Oryza sativa.
            Oryza sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE  1 (bases 1 to 522)
AUTHORS   Dong,H.T., Li,D.B., Zhuang,X.F., Dai,C.G., Sun,L.X., Pei,Y.X., Wu
            ,H.F., Jiang,Y.X., Yu,F.C., Gao,Q.K. and Lou,Y.C.
TITLE     A Gene Expression Screen in Oryza sativa
JOURNAL   Unpublished (2001)
COMMENT   Contact: Dong HT
            Laboratory of Functional Genetics
            Bio-technology Institute of Zhejiang University
            Kaixuan Road 268#, Hangzhou, Zhejiang, P.R.China
            Tel: 0086-571-86892051
            Fax: 0086-571-86961525
            Email: htdong@zjuem.zju.edu.cn
            Seq primer: M13 forward primer.
            Location/Qualifiers
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             M.grisea"
             /tissue_type="leaf"
             /dev_stage="Mature stage"
             /note="Vector: pSport2"
BASE COUNT 138 a 136 c 122 g 126 t
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 2.6e-80;
Matches 443; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1702 AGGTGGTGGCCACCAAGGTGTTCGAGATGCCGCCGTGTCGCGTGGAGGAGCGATGGAG 1761
DB 68 AGGTGGTGGCCACCAAGGTGTTCGAGATGCCGCCGTGTCGCGTGGAGGAGCGATGGAG 127
QY 1762 AGCTAGTGAATGTGGACCAACATCTTACGCTTCAGACAGAGAGAGAGAGAGAGAGATGA 1821
DB 128 AGCTAGTGAATGTGGACCAACATCTTACGCTTCAGACAGAGAGAGAGAGAGAGAGATGA 187
QY 1822 ACCTCTCTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1881
DB 188 ACCTCTCTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 247
QY 1882 ATCTCCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1941
DB 248 ATCTCCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 307
QY 1942 CTCTACACCTCTCTGATCACCATCTCATTTGCTATTTATTTCTATGCTTGTCCCAAGAGT 2001
DB 308 CTCTACACCTCTCTGATCACCATCTCATTTGCTATTTATTTCTATGCTTGTCCCAAGAGT 367
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QY 2002 CTCCTAATATTACTAGTATTAATTAATCAAGTCAGATGAGAGAGGTCTTTGATTGTCTC 2061
Db 368 CTCCTAATATTACTAGTATTAATTAATCAAGTCAGATGAGAGAGGTCTTTGATTGTCTC 427
QY 2062 CGTGTACATCGATCGATCGACTCTTGACVACTCTGTTTAAACCAACTGTTTTCGATATATT 2121
Db 428 CGTGTACATCGATCGATCGACTCTTGACVACTCTGTTTAAACCAACTGTTTTCGATATATT 487
QY 2122 TATATATTAATGATTTTCCAA 2144
Db 488 TATATATTAATGATTTTCCAA 510

RESULT 8
BM420133 534 bp mRNA linear EST 28-JAN-2002
LOCUS R024B06 Oryza sativa mature leaf library induced by M.grisea Oryza
DEFINITION BM420133
ACCESSION BM420133
VERSION BM420133.1 GI:18386935
KEYWORDS EST.
SOURCE Oryza sativa.
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 534)
AUTHORS Dong,H.T., Li,D.B., Zhuang,X.F., Dai,C.G., Sun,L.X., Pei,Y.X., Wu
H.F., Jiang,Y.X., Yu,F.C., Gao,Q.K. and Lou,Y.C.
TITLE A Gene Expression Screen in Oryza sativa
JOURNAL Unpublished (2001)
COMMENT Laboratory of Functional Genetics
Bio-technology Institute of Zhejiang University
Kaixuan Road 268#, Hangzhou, Zhejiang, P.R.China
Tel: 0086-571-86892051
Fax: 0086-571-86961525
Email: htdong@zjuem.zju.edu.cn
Seq primer: M13 forward primer.
FEATURES
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/db_xref="taxon:4530"
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M.grisea"
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/notes="Vector: pSport2"
BASE COUNT 142 a 139 c 127 g 126 t
ORIGIN
Query Match 19.6%; Score 432; DB 13; Length 534;
Best Local Similarity 99.8%; Pred. No. 4.7e-78;
Matches 443; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1702 AGTGTGTCGCACCAAGGTTCAGATCCCGCTCTCGGTGGAGAGCGCATGGAGC 1761
Db 78 AGTGTGTCGCACCAAGGTTCAGATCCCGCTCTCGGTGGAGAGCGCATGGAGC 137
QY 1762 AGCTAGTGAATGACACCAACTTCTACGCCTTCAGAGACGAGAACCGGGAGATGA 1821
Db 138 AGCTAGTGAATGACACCAACTTCTACGCCTTCAGAGACGAGAACCGGGAGATGA 197
QY 1822 ACCTCTCTGTACAGAGAGAGAGAGGCTTCGGTCTCATGCTCCCAAGGAGAGGGTC 1881
Db 198 ACCTCTCTGTACAGAGAGAGAGAGGCTTCGGTCTCATGCTCCCAAGGAGAGGGTC 257
QY 1882 ATCTCCAAAGGAGACCATCCCACTCTGACCAACCCACCCCTCCCTGCTGCTAGC 1941
Db 258 ATCTCCAAAGGAGACCATCCCACTCTGACCAACCCACCCCTCCCTGCTGCTAGC 317
QY 1942 CTCTACACCTCTCTGATCACCACCTCTCTGCTAATTAATTTCTATCTGTCGCCAGAGT 2001

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Db 318 CTCCTACACTCTCTCAACCACTCAATTCCTAATTAATTAATTCATGCTGCCAGAGT 377
QY 2002 CTCCTAATATTACTAGTATTAATTAATCAAGTCAGATGAGAGAGGTCTTTGATTGTCTC 2060
Db 378 CTCCTAATATTACTAGTATTAATTAATCAAGTCAGATGAGAGAGGTCTTTGATTGTCTC 437
QY 2061 CGTGTACATCGATCGATCGACTCTTGACTACTCTGTTTAAACCAACTGTTTTCGATATATT 2120
Db 438 CGTGTACATCGATCGATCGACTCTTGACTACTCTGTTTAAACCAACTGTTTTCGATATATT 497
QY 2121 TTATATTAATTAATGATTTTCCAA 2144
Db 498 TTATATTAATTAATGATTTTCCAA 521

RESULT 9
BQ908495 525 bp mRNA linear EST 19-AUG-2002
LOCUS T008H05 Oryza sativa mature leaf library induced by M.grisea Oryza
DEFINITION BQ908495
ACCESSION BQ908495
VERSION BQ908495.1 GI:22307259
KEYWORDS EST.
SOURCE Oryza sativa.
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 525)
AUTHORS Dong,H.T., Li,D.B., Zhuang,X.F., Dai,C.G., Sun,L.X., Pei,Y.X., Wu
H.F., Jiang,Y.X., Yu,F.C., Gao,Q.K. and Lou,Y.C.
TITLE A Gene Expression Screen in Oryza sativa
JOURNAL Unpublished (2001)
COMMENT Laboratory of Functional Genetics
Bio-technology Institute of Zhejiang University
Kaixuan Road 268#, Hangzhou, Zhejiang, P.R.China
Tel: 0086-571-86892051
Fax: 0086-571-86961525
Email: htdong@zjuem.zju.edu.cn
Seq primer: M13 forward primer.
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location/Qualifiers
source 1. 525
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/db_xref="taxon:4530"
/clone_lib="T008H05"
M.grisea"
/tissue_type="leaf"
/dev_stage="Mature stage"
/notes="Vector: pSport2"
BASE COUNT 142 a 134 c 120 g 128 t 1 others
ORIGIN
Query Match 19.5%; Score 429.4; DB 14; Length 525;
Best Local Similarity 99.3%; Pred. No. 1.6e-77;
Matches 441; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
QY 1702 AGTGTGTCGCACCAAGGTTCAGATCCCGCTCTCGGTGGAGAGCGCATGGAGC 1761
Db 63 AGTGTGTCGCACCAAGGTTCAGATCCCGCTCTCGGTGGAGAGCGCATGGAGC 122
QY 1762 AGCTAGTGAATGACACCAACTTCTACGCCTTCAGAGACGAGAACCGGGAGATG 1820
Db 123 AGCTAGTGAATGACACCAACTTCTACGCCTTCAGAGACGAGAACCGGGAGATG 182
QY 1821 AACGTCCTGTACAGAGAGAGAGAGGCTTCGGTCTCATGCTCCCAAGGAGACCGGT 1880
Db 183 AACGTCCTGTACAGAGAGAGAGAGGCTTCGGTCTCATGCTCCCAAGGAGACCGGT 242
QY 1881 CATCTCCACAGAGAGACCATCCCACTCTGACCAACCCCTCCCTGCTGCTAG 1940

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Db 243 CATCTCCACAGGAGACCATCCCACTCTGACCAACCACCCCTCCCTTGTGCTGCTAG 302
QY 1941 CCTTACACCTCTGCAATCCATCTCTATTTGCTAATATTCTATGCTTGCCCAAGAG 2000
Db 303 CCTTACACCTCTGCAATCCATCTCTATTTGCTAATATTCTATGCTTGCCCAAGAG 362
QY 2001 TCTCTAAATATTACTAGTAAATTAATCAAGTATGATGAGAGAGGCTTTGATTTGCT 2060
Db 363 TCTCTAAATATTACTAGTAAATTAATCAAGTATGATGAGAGAGGCTTTGATTTGCT 422
QY 2061 CCGTGATACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2120
Db 423 CCGTGATACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 482
QY 2121 TTATATTATTATGATTTTCCAA 2144
Db 483 TTATATTATTATGATTTTCCAA 506

RESULT 10
BE230575 460 bp mRNA linear EST 07-JUL-2000
LOCUS 99AS79 Rice Seedling Lambda ZAPII cDNA Library Oryza sativa cDNA
DEFINITION clone 99AS79, mRNA sequence.
ACCESSION BE230575
VERSION BE230575.1 GI:8956772
KEYWORDS EST.
SOURCE Oryza sativa.
ORGANISM Oryza sativa
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
AUTHORS Lee,M.C., Shin,Y.C., Lee,T.H., Jeong,S.H., Kim,J.K., Eun,M.Y. and
Nam,B.H.
TITLE Large-scale Sequencing Analysis of ESTs from Rice Seedling
JOURNAL Unpublished (1999)
COMMENT Contact: Eun M.Y.
Department of Cyto genetics
National Inst. of Agri. Sci. and Tech, RDA
Suwon, Kyunggido, Korea
Tel: 82 331 290 0301
Fax: 82 331 290 0307
Email: myeun@snu20.astro.re.kr.
FEATURES
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/dev_stage="5 days after pollination"
/lab_host="E. coli SOLR"
/notes="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
XhoI; Directional cDNA library inserted into lambda ZAPII
vector at 5' end with EcoRI and 3' end with Xho I site"
BASE COUNT 81 a 161 c 111 g 107 t
ORIGIN
Query Match 19.0%; Score 418.6; DB 10; Length 460;
Best Local Similarity 97.8%; Pred. No. 2.6e-75;
Matches 435; Conservative 0; Mismatches 9; Indels 1; Gaps 1;

QY 1 CGTCGTCGTTTGGCATCCATCCAGAAATCGTTCAGATCCAGCCAGCCAGCATCTC 60
Db 11 CGTCGTCGTTTGGCATCCAGAAATCGTTCAGATCCAGCCAGCCAGCATCTC 70
QY 61 AAGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 120
Db 71 AAGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 130
QY 121 GCGAGACAGACATGTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 180

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Db 131 GCAGAGACAGACATGTTCTTCTTCTAGCTATTAGTGTGGGGAATGAGGCTCCG 190
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Db 191 CCACCAACCGCAGCAATGCGCTCGCGCCGCTCTTCCATCACCATCACCATCACCATG 250
QY 241 TCAGCAGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
Db 251 TCAAGCAGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 310
QY 301 TTGGCGCGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
Db 311 TTGGCGCGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 369
QY 361 GCAGCAGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
Db 370 GCATCATCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 429
QY 421 TTATGACGGCGCGCAAGCTCAAGGT 445
Db 430 TTATGACGGCGCGCAAGCTCAAGGT 454

RESULT 11
BM037750 627 bp mRNA linear EST 06-NOV-2001
LOCUS S098C08 Stem library from Oryza sativa (3-5 leaf stage) Oryza
DEFINITION sativa cDNA clone S098C08, mRNA sequence.
ACCESSION BM037750
VERSION BM037750.1 GI:16753371
KEYWORDS EST.
SOURCE Oryza sativa.
ORGANISM Oryza sativa
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
AUTHORS Dong,H.T., Li,D.B., Zhuang,X.F., Dai,C.G., Sun,L.X., Pei,Y.X., Wu
,H.F., Jiang,Y.X., Yu,F.C., Gao,Q.K. and Lou,Y.C.
TITLE A Gene Expression Screen in Oryza sativa
JOURNAL Unpublished (2001)
COMMENT Contact: Dong HT
Laboratory of Functional Genetics
Bio-technology Institute of Zhejiang University
Kaixuan Road 268#, Hangzhou, Zhejiang, P.R.China
Tel: 0086-571-86892051
Fax: 0086-571-86961525
Email: htdong@zjuem.zju.edu.cn
Seq primer: M13 forward primer.
FEATURES
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/dev_stage="3-5 leaf stage"
/notes="Vector: pSport2"
BASE COUNT 161 a 171 c 145 g 150 t
ORIGIN
Query Match 18.9%; Score 416.8; DB 13; Length 627;
Best Local Similarity 99.1%; Pred. No. 6e-75; 2; Indels 2; Gaps 2;
Matches 440; Conservative 0; Mismatches 0;

QY 1702 AGGTGTGCGCCACCAAGGTGTCAGATGCGCGCGCTGTCGCTGAGAGGCGATGAGC 1761
Db 175 AGGTGTGCGCCACCAAGGTGTCAGATGCGCGCGCTGTCGCTGAGAGGCGATGAGC 234
QY 1762 AGGTGTGAGTGTGAGCAACAACTTCTACGCTTACAGAGAGAGAGACCGGGAGATGA 1821
Db 235 AGGTGTGAGTGTGAGCAACAACTTCTACGCTTACAGAGAGAGAGACCGGGAGATGA 294

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QY	1771	ANGTGGACCACTTCTACGCCITTCAGAGACGAGAGAACCGGGAGATGAACGTCTCCTGT	1830
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QY	1831	ACA-AGAGAGAAGAGGAGCTTGCGTCTCATGTCGCCAAGSGAGAGCGTCATCTCCAC	1889
Dd	121	ACACAGAGAGAAGAGGAGCTTGCGTCTCATGTCGCCAAGSGAGAGCGTCATCTCCAC	180
QY	1890	AAGSAGACATCCCCAACTCTGCACCACACACCCCTCCCTTGCTGCTAGCCTCTACAC	1949
Dd	181	AAGSAGACATCCCCAACTCTGCACCACACACCCCTCCCTTGCTGCTAGCCTCTACAC	240
QY	1950	CCTCTGCATCACCATCCTCATTTGCTTAATTTCATGCTTGCCAGAGTCTCTAAAT	2009
Dd	241	CCTCTGCATCACCATCCTCATTTGCTTAATTTCATGCTTGCCAGAGTCTCTAAAT	300
QY	2010	ATTACTAGTATTAAATCCAAAGTAGAGAGGCTCTTGATTTGTCTCCGCTGAC	2069
Dd	301	ATTACTAGTATTAAATCCAAAGTAGAGAGGCTCTTGATTTGTCTCCGCTGAC	360
QY	2070	TGGATCGATCGACTCTTGACTACTCTGTTTAACCAACCTGTTTCGATATTATTATTAT	2129
Dd	361	TGGATCGATCGACTCTTGACTACTCTGTTTAACCAACCTGTTTCGATATTATTATTAT	420
QY	2130	TAATGATT	2137
Dd	421	TAATGATT	428

Db	421	TAATGATT	428	
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BI811299				
LOCUS		516 bp	mRNA	linear
DEFINITION		N001C12 <i>Oryza sativa</i> mature leaf library induced by <i>M.grisea</i> <i>Oryza sativa</i> cDNA clone N001C12, mRNA sequence.		
ACCESSION		BI811299		
VERSION		BI811299.1	GI:15858487	
KEYWORDS		EST.		
SOURCE		<i>Oryza sativa</i> .		
ORGANISM		<i>Oryza sativa</i>		
		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Eriocaridaceae; Oryzeae; <i>Oryza</i> .		
REFERENCE		1 (bases 1 to 516)		
AUTHORS		Dong,H.T., Li,D.B., Zhuang,X.F., Dai,C.G., Sun,L.X., Pei,Y.X., Wu,H.F., Jiang,Y.X., Yu,F.C., Gao,Q.K. and Lou,Y.C.		
TITLE		A Gene Expression Screen in <i>Oryza sativa</i>		
JOURNAL		Unpublished (2001)		
COMMENT		Contact: Dong HT		

```

tel: 0086-571-86892051
Fax: 0086-571-86361525
Email: htdong@zjuem.zju.edu.cn
Seq primer: M13 forward primer.
Location/Qualifiers
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Db 57 CAAGGTGCGCCACCAAGGTGTTGAGAT--CCCGCTGTGGTGGAGGCGGATCGA-113
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QY 1761 CAGCTAGTGAATGTGACACCAACTTCTACGCCCTTCAGAGAGAGAGAACCGGGGAGATG 1820
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Db 114 CAGCTAGTGAATGTGACACCAACTTCTACGCCCTTCAGAGAGAGAGAACCGGGGAGATG 173
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QY 1821 AACGTCCTGTACAGAGAGAGAGAGAGGCTTCGGTCTCATGTCCTCCCAAGGAGAGAGGT 1880
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Db 174 AACGTCCTGTACAGAGAGAGAGAGAGGCTTCGGTCTCATGTCCTCCCAAGGAGAGAGGT 233
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LOCUS
DEFINITION V006C02 Oryza sativa mature leaf library induced by M.grisea Oryza
sativa cDNA clone V006C02, mRNA sequence.
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ACCESSION BM038608
VERSION BM038608.1 GI:16754229
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KEYWORDS EST.
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SOURCE Oryza sativa.
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ORGANISM Oryza sativa
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REFERENCE
AUTHORS Dong,H.T., Li,D.B., Zhuang,X.F., Dai,C.G., Sun,L.X., Pei,Y.X., Wu
,H.F., Jiang,Y.X., Yu,F.C., Gao,Q.K. and Lou,Y.C.
TITLE A Gene Expression Screen in Oryza sativa
JOURNAL Unpublished (2001)
COMMENT Contact: Dong HT
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REFERENCE
AUTHORS Dong,H.T., Li,D.B., Zhuang,X.F., Dai,C.G., Sun,L.X., Pei,Y.X., Wu
,H.F., Jiang,Y.X., Yu,F.C., Gao,Q.K. and Lou,Y.C.
TITLE A Gene Expression Screen in Oryza sativa
JOURNAL Unpublished (2001)
COMMENT Contact: Dong HT
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REFERENCE
AUTHORS Dong,H.T., Li,D.B., Zhuang,X.F., Dai,C.G., Sun,L.X., Pei,Y.X., Wu
,H.F., Jiang,Y.X., Yu,F.C., Gao,Q.K. and Lou,Y.C.
TITLE A Gene Expression Screen in Oryza sativa
JOURNAL Unpublished (2001)
COMMENT Contact: Dong HT
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QY 1772 TGTGGACCAACAACCTTCTACGCTTCAGAGACGAGAGAGAGAGAGAGAGAGAGAGAGAG 1831
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Db 148 TGTGGACCAACAACCTTCTACGCTTCAGAGACGAGAGAGAGAGAGAGAGAGAGAGAGAG 207
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QY 1832 CAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1891
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QY 1892 GGAGACCATCCCAACTCTGACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 1951
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Db 268 GGAGACCATCCCAACTCTGACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 327
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QY 1952 CCTGCATCACCACCTCTGATGCTATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2011
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Db 328 CCTGCATCACCACCTCTGATGCTATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 387
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QY 2012 TACTAGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2071
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Db 507 ATGATTTTCCAGGTTT 524
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RESULT 15
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BM0906047
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LOCUS
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DEFINITION L010D02 Oryza sativa mature leaf library induced by M.grisea Oryza
sativa cDNA clone L010D02, mRNA sequence.
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ACCESSION BM0906047
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VERSION BM0906047.1 GI:22304825
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KEYWORDS EST.
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SOURCE Oryza sativa.
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ORGANISM Oryza sativa
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REFERENCE
AUTHORS Dong,H.T., Li,D.B., Zhuang,X.F., Dai,C.G., Sun,L.X., Pei,Y.X., Wu
,H.F., Jiang,Y.X., Yu,F.C., Gao,Q.K. and Lou,Y.C.
TITLE A Gene Expression Screen in Oryza sativa
JOURNAL Unpublished (2001)
COMMENT Contact: Dong HT
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REFERENCE
AUTHORS Dong,H.T., Li,D.B., Zhuang,X.F., Dai,C.G., Sun,L.X., Pei,Y.X., Wu
,H.F., Jiang,Y.X., Yu,F.C., Gao,Q.K. and Lou,Y.C.
TITLE A Gene Expression Screen in Oryza sativa
JOURNAL Unpublished (2001)
COMMENT Contact: Dong HT
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REFERENCE
AUTHORS Dong,H.T., Li,D.B., Zhuang,X.F., Dai,C.G., Sun,L.X., Pei,Y.X., Wu
,H.F., Jiang,Y.X., Yu,F.C., Gao,Q.K. and Lou,Y.C.
TITLE A Gene Expression Screen in Oryza sativa
JOURNAL Unpublished (2001)
COMMENT Contact: Dong HT
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REFERENCE
AUTHORS Dong,H.T., Li,D.B., Zhuang,X.F., Dai,C.G., Sun,L.X., Pei,Y.X., Wu
,H.F., Jiang,Y.X., Yu,F.C., Gao,Q.K. and Lou,Y.C.
TITLE A Gene Expression Screen in Oryza sativa
JOURNAL Unpublished (2001)
COMMENT Contact: Dong HT
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Query Match      18.1%; Score 397.4; DB 14; Length 531;
Best Local Similarity 99.5%; Pred. No. 5.6e-71;
Matches 409; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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QY 1762 AGCTAGTGAATGTGAGACCAACTTCTACGCTTCAGAGACGAGAGACCGGGGAGATGA 1821
    |||||
Db 99 AGCTAGTGAATGTGAGACCAACTTCTACGCTTCAGAGACGAGAGACCGGGGAGATGA 158

QY 1822 ACCTCCTGTACAAAGAGAGAGAGGCTTCGGTCTCATCGTCCCAAGGGAGAGCGGTC 1881
    |||||
Db 159 ACCTCCTGTACAAAGAGAGAGAGGCTTCGGTCTCATCGTCCCAAGGGAGAGCGGTC 218

QY 1882 ATCTCCACAGAGAGACATCCCAACTCTGACACACACCCCTCCCTGTGCTGCTAGC 1941
    |||||
Db 219 ATCTCCACAGAGAGACATCCCAACTCTGACACACACCCCTCCCTGTGCTGCTAGC 278

QY 1942 CTCTACACTCCTGTCATCACCCTCATTTGCTTAATTATTCTATGCTTGCCCAAGAGT 2001
    |||||
Db 279 CTCTACACTCCTGTCATCACCCTCATTTGCTTAATTATTCTATGCTTGCCCAAGAGT 338

QY 2002 CTCTAAATATTACTAGTATTAAATTAATCAAGTGTATGAGAGAGTCTTTGATTGTCTC 2061
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Db 339 CTCTAAATATTACTAGTATTAAATTAATCAAGTGTATGAGAGAGTCTTTGATTGTCTC 398

QY 2062 CGTGTACATCGATCGACGACTCTTGACTACTCTGTTTAAACCAACTGTTT 2112
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Db 399 CGTGTACATCGATCGACGACTCTTGACTACTCTGTTTAAACCAACTGTTT 449

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Search completed: March 26, 2003, 07:52:29
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GenCore version 5.1.4.p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 26, 2003, 04:38:30 ; Search time 54.4409 Seconds
(without alignments)
12398.686 Million cell updates/sec

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Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	74.2	3.4	7218	1	US-08-232-463-14
5	62.2	2.8	636	4	US-08-998-416-1137
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8	58.8	2.7	2317	4	US-09-105-390-3
9	58.4	2.7	615	4	US-08-998-416-186
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11	56	2.5	837	4	US-08-998-416-288
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13	51.2	2.3	6124	4	US-08-213-419B-3
14	50.8	2.3	1140	3	US-09-023-173-4
15	50.6	2.3	19124	2	US-08-487-826B-13
16	50	2.3	665	2	US-08-883-795A-36
17	49.2	2.2	837	4	US-08-998-416-288
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19	49.2	2.2	1926	4	US-09-249-585A-4
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22	49.2	2.2	15079	4	US-09-385-028-1
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24	49	2.2	33529	4	US-09-144-085-3
25	48.4	2.2	19124	2	US-08-487-826B-13
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27	48	2.2	2787	4	US-09-105-537-40

28	48	2.2	5970	3	US-09-320-878-21
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30	47.8	2.2	828	4	US-08-998-416-538
31	47.8	2.2	4403765	4	US-09-103-840A-2
32	47.6	2.2	1072	1	US-07-971-096-1
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34	47.6	2.2	168575	1	US-09-426-290-1
35	47.4	2.2	3546	1	US-07-951-715A-14
36	47.4	2.2	3546	2	US-08-459-448A-14
37	47.4	2.2	3546	3	US-08-459-595A-14
38	47.4	2.2	3546	3	US-08-459-504B-14
39	47.4	2.2	3546	3	US-08-459-444-14
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41	47	2.1	3468	1	US-07-951-715A-2
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43	47	2.1	3468	2	US-08-459-448A-2
44	47	2.1	3468	2	US-08-459-448A-4
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ALIGNMENTS

RESULT 1
US-08-728-956-3
; Sequence 3, Application US/08728956
; Patent No. 5677175
; GENERAL INFORMATION:
; APPLICANT: Hodges, Thomas K.
; APPLICANT: McGee, J. D.
; TITLE OF INVENTION: Plant Pathogen Induced Proteins
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Barnes & Thornburg
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: USA
; ZIP: 46204
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/728,956
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Breen, John P.
; REGISTRATION NUMBER: 38,833
; REFERENCE/DOCKET NUMBER: 3220-26119
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317)231-7745
; TELEFAX: (317)231-7433
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1591 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Oryza sativa
US-08-728-956-3

Query Match 4.2%; Score 91.4; DB 1; Length 1591;
Best Local Similarity 66.9%; Pred. No. 8.4e-12;
Matches 164; Conservative 0; Mismatches 71; Indels 10; Gaps 2;
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/     STRANDEDNESS: single
/     TOPOLOGY: linear
/     MOLECULE TYPE: DNA (genomic)
/     ORIGINAL SOURCE:
/         ORGANISM: PAG1074RP
/         US-08-998-416-186

```

Query Match 2.7%; Score 58.4; DB 4; Length 615;
Best Local Similarity 47.9%; Pred. No. 0.00023;
Matches 230; Conservative 0; Mismatches 246; Indels

2:

[illegible]

```

RESULT 10
US-09-197-649-7
; Sequence 7, Application US/09197649
; Patent No. 6194550
; GENERAL INFORMATION:
; APPLICANT: Gold, Larry
; APPLICANT: Tuerk, Craig
; APPLICANT: Pribnow, David
; APPLICANT: Smith, Jonathan D.
; TITLE OF INVENTION: Systematic Polypeptide Evolution by Reverse Translation
; FILE REFERENCE: NEX02/C1-CON
; CURRENT APPLICATION NUMBER: US/09/197,649
; CURRENT FILING DATE: 1998-11-23
; EARLIER APPLICATION NUMBER: 07/829,461
; EARLIER FILING DATE: 1992-01-31
; EARLIER APPLICATION NUMBER: 07/739,055
; EARLIER FILING DATE: 1991-08-01
; EARLIER APPLICATION NUMBER: 07/561,968
; EARLIER FILING DATE: 1990-08-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 7
; LENGTH: 390
; TYPE: DNA

```

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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Sequence
; OTHER INFORMATION: having a 120 repeat of ACG flanked by fixed
; OTHER INFORMATION: fragments having NcoI restriction sites.
US-09-197-649-7

Query Match          2.6%; Score 56.6; DB 4; Length 390;
Best Local Similarity 51.0%; Pred. No. 0.00048;
Matches 134; Conservative 0; Mismatches 129; Indels 0; Gaps

QY 1372 CCACGCGGTATCCGCGCGGAGGAGGACGCCAGTCCACATGACCGACATPCGACCTGCG 1431
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 128 CGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGA 187
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1432 CTCCTCATCATCAAGAGGAAAGTCTAGGAAAGATCAAGAGAGAGGAGACCGACGTCGCGCA 1491
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 188 CGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGA 247
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1492 CCTCAAGGGGACCAAGGCCCGCTCCGAGCTGGCGCCCATCTTGTCTGACACAACAGA 1551
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 248 CGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGA 307
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1552 CGACGACGCCACAGGCCCGCTCAAGGATCTGGAGAGGCCGCTCGCGCGGAGGACGAGGA 1611
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 308 CGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGA 367
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 1612 CACGGTGCTCACCAAGGTTGTCA 1634
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 368 CGCCATGTTGGGATGTTGCAGA 390
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

RESULT 11
US-08-998-416-288
; Sequence 288, Application US/08998416
; Patent No. 6239264
; GENERAL INFORMATION:
; APPLICANT: Philippsen, Peter
; APPLICANT: Pohlmann, Rainer
; APPLICANT: Steiner, Sabine
; APPLICANT: Mohr, Christine
; APPLICANT: Wendland, Jorgen
; APPLICANT: Knechtle, Philipp
; APPLICANT: Rebischung, Corinne
; TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSYPII
; NUMBER OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 1152
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NO. 6239264artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NO. 6239464th Carolina
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/998,416
; FILING DATE: 24-DEC-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: CH 0016/97
; FILING DATE: 31-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Weigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8669


```

CORRESPONDENCE ADDRESS:
ADDRESSER: Knobbe Martens Olson & Bear
STREET: 620 Newport Center Drive 14th Floor
CITY: Newport Beach
STATE: California
COUNTRY: US
Zip: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,826B
; FILING DATE: 10-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelsen, Ned
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: NIH121.001CPI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19124 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; US-08-487-826B-13

Query Match      2.3%; Score 50.6; DB 2; Length 19124;
Best Local Similarity 44.8%; Pred. No. 0.074;
Matches 236; Conservative 0; Mismatches 289; Indels 2; Gaps 1;

QY 476 TTCCCTGGAAATTCCTCGTTCTATATATAGAGTTTCTAGCATTTACTCATATTCACAT 535
Db 16231 TTCCACACAGATGTTGGTTTCTTCTAAAAAAGAAATGAACATATATGCTGTATGTA 16172

QY 536 ATATATATATATAGATATATCTAGATTCATTTATCATATATATATATATAGTAAATGCTA 595
Db 16171 ATATGATATATATATATATATGTTTCTTAAATGATATATATGATGATGATGATGATG 16112

QY 596 GAAATCTTAAACCTGAAACAGAGGAGATATATATATATGTTGGAATGGAACATGAGAT 655
Db 16111 TATATATATATATATATATATATATATATATGATGTAATGTAATGTAATGTAATG 16052

QY 656 TTGTTTATATATGACCTTTATGAAATATCTAGTAGATTCACGAACTACATTCCTTC 715
Db 16051 ATATATATATATATATATGATGTAATGTTGTAATGTTGTAATGTTGTAATGTTGTA 15992

QY 716 TTTATGTTATATATATAGATATATTTGCTTCACTAGATTCCTATTTTATATCT--AGAGAG 773
Db 15991 TATGTAATGATATATGCAATGTAATATTTATTTTATTTTATTTTATTTTATTTTAT 15932

QY 774 ATTTAAATATATATACAACTACCTGATATACCCGTTGCAACGGAATAGTATATGACCT 833
Db 15931 TTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 15872

QY 834 ATTTATTTATTTATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 893
Db 15871 ATTTATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 15812

QY 894 TGACATTCCTCTATATATATATATATATATATATATATATATATATATATATATATAT 953
Db 15811 AAATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 15752

QY 954 TCGTCATCAATATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 1000
Db 15751 TATGATATATATATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 15705
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Search completed: March 26, 2003, 13:11:56
Job time : 246.441 secs

C	1	143.6	6.5	2000	10	US-09-887-576-859	Sequence 859, Appl
C	2	124.4	5.7	356	10	US-09-770-791-606	Sequence 606, Appl
C	3	110.2	5.0	689	10	US-09-770-791-308	Sequence 308, Appl
C	4	100.4	4.5	33675	10	US-09-921-932-2	Sequence 2, Appl
C	5	97.4	4.4	2000	10	US-09-887-576-832	Sequence 832, Appl
C	6	96.6	4.4	2000	10	US-09-887-576-859	Sequence 859, Appl
C	7	92.8	4.2	2000	10	US-09-887-576-862	Sequence 862, Appl
C	8	72.6	3.3	33675	10	US-09-921-932-2	Sequence 2, Appl
C	9	72.4	3.3	2000	10	US-09-887-576-832	Sequence 832, Appl
C	10	59.6	2.7	550	10	US-09-791-171-63	Sequence 63, Appl
C	11	56.5	2.6	390	9	US-09-790-399-7	Sequence 7, Appl
C	12	53.4	2.4	2000	9	US-09-938-842A-4849	Sequence 4849, Ap
C	13	51.6	2.3	2520	9	US-09-838-529A-9	Sequence 9, Appl
C	14	51.4	2.3	640681	10	US-09-790-988-1	Sequence 1, Appl
C	15	49.2	2.2	4880	9	US-09-927-827-35	Sequence 35, Appl
C	16	49	2.2	2000	9	US-09-938-842A-3436	Sequence 3436, Ap
C	17	48.8	2.2	516	10	US-09-960-352-5785	Sequence 5785, Ap
C	18	48.8	2.2	3624	10	US-09-927-112-3	Sequence 3, Appl
C	19	48.8	2.2	4635	10	US-09-927-112-1	Sequence 1, Appl

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Db      44 CTGAGGAATCAAGGAGAAGGCACGAG 15
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RESULT 3
US-09-770-149-308
; Sequence 308, Application US/09770149
; Patent No. US20020059663A1
; GENERAL INFORMATION:
; APPLICANT: Goriach, Jörn
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Matthew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Woessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Krieker, MaJa
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Hurban, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; FILE REFERENCE: thaliana
; FILE REFERENCE: 2024 (PARA-013PRV)
; CURRENT APPLICATION NUMBER: US/09/770.149
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,506
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 308
; LENGTH: 689
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(689)
; OTHER INFORMATION: n = A,T,C or G
US-09-770-149-308

Query Match          5.0%; Score 110.2; DB 10; Length 689;
Best Local Similarity 62.2%; Pred. No. 2.2e-16;
Matches 163; Conservative 0; Mismatches 99; Indels 0; Gaps

QY   1214 GAGAAGGTGAAGAGCACATCGAGGAGAGAGCGGGGAGAGCAGTGGCGAAGCACACGCCAG 12733
      ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    362 GAGCCAATTAAAGCAGCATGTTGAAGAGAAGTAGGCAAATCTGTTTCAGAAACACACAGTCAT 421

QY   1274 CTTCTGAAGGSGTGAGCGTCGCCCTCTCCGCCGCGGTGGGAGACTCCAGCCGAGGTGCC 13333
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    422 CTTGTGAGAGAAGTTGATGTAAAGACTCTCTGTTCTGTGGTGAGAGCTTTGGTAAGGCCCT 481

QY   1334 AAGATTTCAGGTGCGAGATCACTCTTTCACCAGGCCAGCGCGGTGCATCCGCGGCCGAG 13933
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    482 AGGATTCGAAGATGTGAGGTGACATGTTTCAAGAAGACATGGTGTGTTGTCGTGTGAG 541

QY   1394 GAGACGCGGAGTCCACCTACGCCACATCAACCTCGCTTCCTCCATCATCATCAGAGGAG 14533
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    542 GAAGATCTGTAGACAGTATACGGTTGTATFCGACTTGGTATCAACGATAATACAGAGGAG 601

QY   1454 CTCAGGAATCAAGGAGAAGG 1475
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    602 CTGAGGAGAGANNNNNNNNG 623

RESULT 4

```

```
US-09-921-992-2/c
; Sequence 2, Application US/09921992
; Patent No. US20020069426A1
; GENERAL INFORMATION:
; APPLICANT: Boronot, Albert;
; APPLICANT: Campos, Narciso;
; APPLICANT: Rodriguez-Concepcion, Manuel;
; APPLICANT: Seeman, Myriam;
; APPLICANT: Valentín, Henry E.;
; APPLICANT: Venkatesh, Tyamagondlu V.;
; APPLICANT: Venkatesh, Mylavaraou
; TITLE OF INVENTION: methyl-D-erythritol phosphate pathway genes
; FILE REFERENCE: 16516.107/35-21(51897)US
; CURRENT APPLICATION NUMBER: US/09/921,992
; CURRENT FILING DATE: 2001-06-25
; PRIOR FILING DATE: 2000-08-06
; PRIOR APPLICATION NUMBER: US 60/223,483
; NUMBER OF SEQ ID NOS: 85
; SEQ ID NO 2
; LENGTH: 33675
; TYPE: DNA
; ORGANISM: Oryza sativa
; NAME/KEY: CDS
; LOCATION: (6924)..(7019), (7163)..(7269), (7344)..(7444), (7525)..(7634),
; LOCATION: (7694)..(7813), (7923)..(8153), (8253)..(8369), (8515)..(8583),
; LOCATION: (9012)..(9071), (9163)..(9225), (9228)..(9472), (9589)..(9730),
; LOCATION: (9951)..(10028), (10134)..(10293), (10694)..(10798),
; LOCATION: (11028)..(11129)
; NAME/KEY: unsure
; LOCATION: (1..33675)
; OTHER INFORMATION: unsure at all n locations
US-09-921-992-2

Query Match      4.5%; Score 100; DB 10; Length 33675;
Best Local Similarity 67.6%; Pred. No. 9.5e-13;
Matches 173; Conservative 0; Mismatches 75; Indels 8; Gaps 2;

QY 843 TACTACCTCCATATTTATGATGACGCGCTTCACCTTTTCTCCACGTTTGACCATTC 902
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 16817 TACTCCCTCCGTTCTPAAATATTCATGCGGTTGACTTTTTTAAACAGTTTGACCGTTC 16758

QY 903 GTCTATTAAAAAATATGATCTATCTATTTATTTATTTATTTATGATCTGATCTCATCA 962
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 16757 GTCTATTCAAAATTTAAATAAGTATATTT-TTTTCTATCATTTGATTCATTGTTA 16699

QY 963 AATATTTTAAACATGACATACATTTTCATATTTGCAAAA-----AAAAAAGC 1015
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 16698 AATATCTTTTATGATACATATAGTTTATATATTTTCACAAAAATTTTGAATAGATG 16639

QY 1016 AATGTCAAATGTTAGTCGAAAGTCATGCTGTCATACATTAATAATACGAGGATTTAT 1075
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 16638 AATGTCAAACATGCTCAAAAGTAAAGTAAAGTAAAGTAAATTTAGAACGAGGAGTAT 16579

QY 1076 ATGGGATGATCAGT 1091
      || || || || ||
Db 16578 ATCCGTATCTATCGT 16563

RESULT 5
US-09-887-576-832/c
; Sequence 832, Application US/09887576
; Patent No. US20020144047A1
; GENERAL INFORMATION:
; APPLICANT: Budworth, P.
; APPLICANT: Brown, D.
; APPLICANT: Chang, H.
; APPLICANT: Zhu, T.
; APPLICANT: Han, B.
; APPLICANT: Wang, X.
; APPLICANT: Cooper, Bret
; TITLE OF INVENTION: Promoters for regulation of plant expression

US-09-887-576-859
; Sequence 859, Application US/09887576
; Patent No. US20020144047A1
; GENERAL INFORMATION:
; APPLICANT: Budworth, P.
; APPLICANT: Brown, D.
; APPLICANT: Chang, H.
; APPLICANT: Zhu, T.
; APPLICANT: Han, B.
; APPLICANT: Wang, X.
; APPLICANT: Cooper, Bret
; TITLE OF INVENTION: Promoters for regulation of plant expression

FILE REFERENCE: 1360.001US1
CURRENT APPLICATION NUMBER: US/09/887,576
CURRENT FILING DATE: 2001-06-25
PRIOR APPLICATION NUMBER: US 60/213,848
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: US 60/214,087
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: US 60/258,692
PRIOR FILING DATE: 2000-12-29
NUMBER OF SEQ ID NOS: 875
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 859
LENGTH: 2000
TYPE: DNA
ORGANISM: Oryza sativa
US-09-887-576-859

Query Match      4.4%; Score 96.6; DB 10; Length 2000;
Best Local Similarity 63.1%; Pred. No. 5.4e-13;
Matches 185; Conservative 0; Mismatches 101; Indels 7; Gaps 2;

QY 820 AGTAATATGAGACCTATTACTTACTACCTCCATTTTAAATGATGACGCGTCTACT 879
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1781 ATTATTTTGGACCCGAGAGAGTACTTCTCCGTCCTAAATATTGACACCATTCATT 1722

QY 880 TTTTGCCACGCTTTGGACCATTCCTCTTATTAAATAAAATATCTATCTATTTATTT 939
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1721 TTTTAAACATGTTTGACCGCTTCCTTATCAAAAATTAAGTAAATTAATTAATTTT 1653

QY 940 TATTATGACTTGATTCGTCATCAATATTTTAAAGCATGACATCAACATTTTCATATT 999
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1662 TTCTATCATTTGATTCATTTAAATATATTTTCCGTATATATATAGTTTCATATTT 1603

QY 1000 CAAAA-----AAAAAACGATGCTCAATGTTAGTCTGAAAGTCATGCTCATATA 1053
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1602 ACATTAAGTTTAAATAAGAGATGCTCAAAATGTTTAAAGATCAACACGTCATA 1543

QY 1054 CATTAATAATGAGGAGGATATATGAGTACGATAGTACAGTAGCAGAGTCATGATA 1106
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1542 TATTAGGACGAGGAGGATATATGTTAGTACATCCGTCGCGAAATAATTTA 1490

RESULT 6
US-09-887-576-859
; Sequence 859, Application US/09887576
; Patent No. US20020144047A1
; GENERAL INFORMATION:
; APPLICANT: Budworth, P.
; APPLICANT: Brown, D.
; APPLICANT: Chang, H.
; APPLICANT: Zhu, T.
; APPLICANT: Han, B.
; APPLICANT: Wang, X.
; APPLICANT: Cooper, Bret
; TITLE OF INVENTION: Promoters for regulation of plant expression

FILE REFERENCE: 1360.001US1
CURRENT APPLICATION NUMBER: US/09/887,576
CURRENT FILING DATE: 2001-06-25
PRIOR APPLICATION NUMBER: US 60/213,848
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: US 60/214,087
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: US 60/258,692
PRIOR FILING DATE: 2000-12-29
NUMBER OF SEQ ID NOS: 875
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 859
LENGTH: 2000
TYPE: DNA
ORGANISM: Oryza sativa
US-09-887-576-859

Query Match      4.4%; Score 96.6; DB 10; Length 2000;
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QY 1076 AT 1077
 Db 1327 AT 1328

RESULT 8
 US-09-921-992-2
 ; Sequence 2, Application US/09921992
 ; Patent No. US20020069426A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Campos, Narciso;
 ; APPLICANT: Boronat, Albert;
 ; APPLICANT: Rodriguez-Concepcion, Manuel;
 ; APPLICANT: Rohmer, Michel;
 ; APPLICANT: Seeman, Myriam;
 ; APPLICANT: Valentin, Henry E.;
 ; APPLICANT: Venkatesh, Tyamagondlu V.;
 ; APPLICANT: Venkatesh, Mylavaram;
 ; TITLE OF INVENTION: Methyl-D-Erythritol phosphate Pathway Genes
 ; FILE REFERENCE: 16516.107/35-21(51897)US
 ; CURRENT APPLICATION NUMBER: US/09/921,992
 ; CURRENT FILING DATE: 2001-08-06
 ; PRIOR APPLICATION NUMBER: US 60/223,483
 ; PRIOR FILING DATE: 2000-08-07
 ; NUMBER OF SEQ ID NOS: 85
 ; SEQ ID NO 2
 ; LENGTH: 33675
 ; TYPE: DNA
 ; ORGANISM: Oryza sativa
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (6924)..(7019), (7163)..(7269), (7344)..(7444), (7525)..(7634),
 ; LOCATION: (7694)..(7813), (7923)..(8153), (8253)..(8369), (8515)..(8589),
 ; LOCATION: (9012)..(9071), (9163)..(9225), (9328)..(9472), (9589)..(9730),
 ; LOCATION: (9951)..(10028), (10134)..(10293), (10694)..(10798),
 ; LOCATION: (11028)..(11129),
 ; NAME/KEY: unsure
 ; LOCATION: (1..33675)
 ; OTHER INFORMATION: unsure at all n locations
 US-09-921-992-2

Query Match 3.3%; Score 72.6; DB 10; Length 33675;
 Best Local Similarity 59.2%; Pred. No. 3.3e-06;
 Matches 145; Conservative 0; Mismatches 94; Indels 6; Gaps 1;

QY 843 TACTACCTCCATATTATTATGATGACCGGTCACATTTTGTCTCCACGTTGACCATTC 902
 Db 16580 TACTCTCCGCTTCATAATATTATACACCGTTACCTTTTATGACATGTTGACCATTC 16639
 QY 903 GTCCTATTAAAAAATTATGATCTATTTATTTATTTATGACTTGTGTCATCA 962
 Db 16640 ATCTATTCAAAATTTTGTGCAATATATAAAACATATGATATACATAAAGTATATT 16699
 QY 963 AATAATTTTAAAGCATCAATCAATTAACATTTTCATATTGCAAAAAA-----AAAAAACGA 1016
 Db 16700 AACATGAATCAAAATGATAGGAAAAAATAATACTATTAAAAATTTTGAATAAGACGA 16759
 QY 1017 ATGTCCTAAATGTTAGTCGAAAGTCAATGGTGTCAACATTAATAACGAGGGATATA 1076
 Db 16760 ACGGTCAACATGTTTAAAAAAGTCAACGCGATCGAATATTAGAAACGAGGGAGTATA 16819
 QY 1077 TGGGA 1081
 Db 16820 TGAGA 16824

RESULT 9
 US-09-887-576-832
 ; Sequence 832, Application US/09887576
 ; Patent No. US20020144047A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Budworth, P.

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 25, 2003, 18:27:39 ; Search time 361.22 Seconds
(without alignments)
14774.266 Million cell updates/sec

Title: US-09-702-134-7212_COPY_28000_30500
Perfect score: 2501
Sequence: 1 atgtccagataaaattggc.....ctatcaatggtgttcatt 2501

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125995159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_101002.*

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- 23: /SID82/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
- 24: /SID82/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	292.4	11.7	1259	16	AAQ75360
2	282.4	11.7	1259	22	AAQ75360
3	290.8	11.6	1169	21	AAQ75361
4	271	10.8	1490	16	AAQ75361
5	229.6	9.2	1420	24	AAQ75361
6	228	9.1	1395	16	AAQ75359
7	226.4	9.1	1161	21	AAQ75359
8	174	7.0	1122	22	AAQ75356
9	153.2	6.1	1077	21	AAQ75361

10	129	5.2	811	21	AAZ99478
11	126.4	5.1	2112	22	AAH46558
12	114.8	4.6	1187	22	AAH46555
13	94.4	3.8	799	19	AAV55831
14	94.4	3.8	1926	21	AAH50254
15	94.4	3.8	1926	22	AAH50254
16	94.4	3.8	2580	21	AAH75454
17	94.4	3.8	2580	24	AAH75454
18	94.4	3.8	5452	20	AAH90923
19	94.4	3.8	8705	20	AAZ23778
20	94.4	3.8	9600	19	AAV21683
21	94.4	3.8	10380	20	AAZ22248
22	94.4	3.8	10596	14	AAQ51731
23	94.4	3.8	10596	17	AAH40348
24	94.4	3.8	10596	20	AAH15650
25	94.4	3.8	16080	21	AAH59553
26	94.2	3.8	1181	20	AAH27502
27	94.2	3.8	1181	22	AAH09902
28	94	3.8	114793	22	AAH08215
29	92.8	3.7	1925	20	AAH90924
30	92	3.7	8298	22	AAH72613
31	89	3.6	7720	21	AAH53800
32	85.8	3.4	1000	21	AAH02484
33	84.4	3.4	795	19	AAH55830
34	83.6	3.3	1948	22	AAH46557
35	79.8	3.2	1505	15	AAQ55750
36	79.2	3.2	2744	16	AAH98470
37	77.2	3.1	672	24	AAH59991
38	76.2	3.0	1274	21	AAH33593
39	75.4	3.0	174	16	AAH75364
40	74.2	3.0	1105	20	AAH04613
41	74.2	3.0	1690	20	AAH04614
42	74.2	3.0	114955	20	AAH53491
43	73.2	2.9	276	24	AAH75810
44	73	2.9	446	22	AAH50433
45	73	2.9	446	22	AAH68382

ALIGNMENTS

RESULT 1	AAQ75360	standard; cDNA to mRNA; 1259 BP.
XX	AAQ75360;	
AC	AAQ75360;	
XX		
DT	01-JUL-1995	(first entry)
DE	Gibberellin-20-oxidase.	
XX	Gibberellin-20-oxidase; plasmid pat2301; transgenic plant;	
KW	Gibberellin-20-oxidase; plasmid pat2301; transgenic plant;	
KW	crop improvement; ss.	
XX		
OS	Arabidopsis thaliana.	
XX		
PH	Key	Location/Qualifiers
FT	CDS	12..1142
FT		/*tag= a
FT		/note= "GA-20-oxidase"
PN	W09428141-A.	
XX		
PD	08-DEC-1994.	
XX		
PF	24-MAY-1994;	94WO-EP01664.
XX		
PR	28-MAY-1993;	93GB-0011147.
XX		
PA	(LONG-) LONG ASHTON RES STATION.	
XX		
PI	Graebe JE, Hedden P, Lange T, Phillips A;	
XX		

Db 906 AAGAGCTGCTTGCACCGGGCGGTGGTGAACAGCAAGAGCGAGAGGAAGTCACTTGCAATC 965

SQ Sec

Query Match	11.7%;	Score 292.4;	DB 22;	Length 1259;
Best Local Similarity	60.0%;	Pred. No. 1.2e-48;		
Matches 532;	Conservative 0;	Mismatches 336;	Indels 18;	Gaps 2;
QY	939	GAGCGTCGAGAGAGCGCGCTCTTCCTGCTGGTTAAACAGCGCATCGAGCGCGCGTC	998	
Db	264	GAGCGCTGTAAAGACGCGGTTCTCTCTGCTGGTCAATCAACGCGCATCGAGGAGGCTT	323	
QY	999	CTGGAGGAGCGCACCGGTGCATGACGCGCTTCTCACGCTCGCGTGGGGGAGAGCA	1058	
Db	324	ATATCAGAGCGCTCATGAATACAGAGCGGCTTTTGTATAGCTCTCTCCGAAACAC	383	
QY	1059	CGGCGCACGCGCGCGGGAGAGCTCGGGGTACGCCAGCAGCTTCACGGCGCGCTTC	1118	
Db	384	AGGGCTTTAGAAATCCGCTGAGAGTGTGGCTACGCAAGCAGTTTACCGGACGCTTC	443	
QY	1119	CGCTCCAGCGCTCGCTGGAGAGAGCGCTGTCTGCTCCGCTACTCATCGCTGGAGATGA	1178	
Db	444	TCCACCAAGCTTCCATGSAAGAGAGCCCTTTCTTTTCGGT-----TTTGCAGCAC	494	
QY	1179	GAGGGCGAGAGGGCGGTGGGTAGTACCTGTGTGGGAAGCTGGGGCGGAGACGGCGG	1238	
Db	495	ATGAGCGGCTCAAAATCCGTTCAAGATTACTTCTGCGATGCGTTGGACATGGGTTTCAG	554	
QY	1239	CGGCTGGGCGAGGTGTACTCGCGCTACTGTCACAGAGATGAGCGCGCTGTGCTGGAGCTG	1298	
Db	555	CCATTTGGGAAGGTGTATCAAGAGTATTGTGAAGCAATGAGTTCTCTATCATTTGAAGATC	614	
QY	1299	ATGGAGGTCGTCGGGAGAGCGCTGGGCGATGCTGGGAGACCGGCGCCACTACTTCCGGCGA	1358	
Db	615	ATGAGGCTTCGCGGCTAAGTTTAGCC-----GTAAACGGGACTACTTTAGAGAG	665	
QY	1359	TTCTTCCAGCGCAAGCACTCCATCATGTGGCGCTCAACTACTACCGGCGGTCCGACAGGCCA	1418	
Db	666	TTTTTTCGAAAGAAACGATTCAATATATGAGACTGAATTACTACCTTCCATGTATAAAACCA	725	
QY	1419	CTGACACGCTGGGACCGGCTCGGACGTGCGACGCCACCCACTGCTCACCACTCCACACAG	1478	
Db	726	GATCTCACACTAGAACAGAACCTCATTTGTATGACACATCTCTTACCATCTCTTACCAAA	785	
QY	1479	GACCACTCGCGCGCTGGAGGTGTGGCGGAGGGCGGTGGCGGGCATCCGCGCTCGC	1538	
Db	786	GACCATGTTAATGGCGCTCAAGTCTTTGTGGAATCAATGCGCTCATCTGTCGCCAAC	845	
QY	1539	CCGGGGCGCTCGTCTGACGTGCGGACACCTTATATGGCGCTCTCCACGCCAGGTAC	1598	
Db	846	CCCAGGCGCTTTGGTGCAATATCGGCGATACTTTTCATGGCTCTATGACAGATAGATAC	905	
QY	1599	CGCAGTGTGCTGCACCGGGCGGTGCTCAACAGCACGGCGGCTTCGCGCGCTCGTGGCGCTTC	1658	
Db	906	AAGAGCTGTTCACCGGCGGTGTGAACAGCAAGAGCGAGAGGAAGTCACTTGCATTC	965	
QY	1659	TTCTCTGCGCGGAGAGGACAGCTGTGTGGCGCCCGCGGAGAGCTGGTCTGACAGCAC	1718	
Db	966	TTCTTGTGTCCGAAAGACAGATGATGTAGCGCCACCGAGAGAGCTTTTGGACAGATC	1025	
QY	1719	CACCGGAGGGGTATCCCGGACTTCAGTGGGGCGGCTGCTGGACTTCACGACAGCGCAC	1778	
Db	1026	ACATCAAGAAGATACCTGACTTCATCATGGTCTATGTCTTGTGATTCACTCAGAACAT	1085	
QY	1779	TACAGGCGCGACATGCGCACGCTTTCAGGCGCTTCTCGACTGCGCTTA	1824	
Db	1086	TATAGACGACATGAACACTCTCCAGCGCTTTTCAGATTGGCTCA	1131	

RESULTS

AAC42398

ID	AAC42398 standard; DNA; 1169 BP.
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XX

AAC42398;

XX
DT 17-OCT-2000 (first entry)

PR 21-JUN-1999; 99US-0139817.
 PR 22-JUN-1999; 99US-0139899.
 PR 23-JUN-1999; 99US-0140353.
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 PR 24-JUN-1999; 99US-0140695.
 PR 28-JUN-1999; 99US-0140823.
 PR 29-JUN-1999; 99US-0140991.
 PR 30-JUN-1999; 99US-0141287.
 PR 01-JUL-1999; 99US-0141842.
 PR 01-JUL-1999; 99US-0142154.
 PR 02-JUL-1999; 99US-0142055.
 PR 06-JUL-1999; 99US-0142390.
 PR 08-JUL-1999; 99US-0142803.
 PR 09-JUL-1999; 99US-0142920.
 PR 12-JUL-1999; 99US-0142977.
 PR 13-JUL-1999; 99US-0143542.
 PR 14-JUL-1999; 99US-0143542.
 PR 15-JUL-1999; 99US-0144005.
 PR 16-JUL-1999; 99US-0144085.
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 PR 19-JUL-1999; 99US-0144321.
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 PR 19-JUL-1999; 99US-0144333.
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Query Match 11.6%; Score 290.8; DB 21; Length 1169;
 Best Local Similarity 59.9%; Pred. No. 2.4e-48;
 Matches 531; Conservative 0; Mismatches 337; Indels 18; Gaps 2;
 QY 939 GAGGCGTCGAGAGGACGCTCTCTCTGCTTAAACACGCGATCGAGCGCGCTG 998
 Db 288 GAGGCGCTGAAGAGCAGCGCTTCTCTCTGCTCAATCATCGCATCAGGAGGCTT 347
 QY 999 CTGAGGAGGCGCACGCTGCTGCTTCTTCTACGCTGCGCTGGGGGAGAGCAG 1058
 Db 348 ATTTCAGACGCTCATGAATACAGAGCGCGCTTCTTGTATGCTCTCTCCGAAACAG 407
 QY 1059 CGGGCGCAGCGCGCGGGGAGAGCTGCGGCTACGCCAGACAGCTTACGGGGCGCTC 1118
 Db 408 AGGGTCTCTAGAAAATCCGCTGAGAGTGTGGCTAOCGAAGCAGTTTCAACGCGCTTC 467
 QY 1119 GCGTCCAGCTCGCTGGAGAGAGCGCTGCTTCTCGGTACTCATCGCTGGAGATGAA 1178
 Db 468 TCACCAAGCTTCCATGGAAGAGACCGCTTCTTTCGCGT-----TTTGCAGAC 518
 QY 1179 GAGGCGGAGGAGGCGCTGCTGAGTACCTGGTGGGAGAGCTCGGGGCGGAGCACGGGG 1238
 Db 519 ATGAGCCGCTCAAAATCCGCTTCAAGTACTTCTGCGATCGCTTGGACATGGGTTTCAG 578

QY	1239	CGGCTGGGCGAGGTGTA	CTCGGCTACTG	CCACAGATGAGCGGCGCTGTGCTGGAGCTG	1298
Db	579	CCATTTGGGAAGGTGTAT	CAAGAGTATTST	TGAAGCAATGAGTTCCTCTATCACTGAAGATC	638
QY	1299	ATGGAGGTGCTGGGAGAGCCT	TGGGACGTGTGGAGACCGGCGCCACTACTTCTCCGGGA	1358	
Db	639	ATGAGCTTCTGGGCTAAGTT	TAGGC-----GTAAACGGGACTACTTCTTAGAG	689	
QY	1359	TTCCTTCAGCGCAACGACT	CCATCAATGCGCTCAACTACTACCGGGGTGCCAGAGGCCA	1418	
Db	690	TTTTTCAAGAAACAGTATT	CAATAATGAGACTGAATTACTACCTCCATGATAAACC	749	
QY	1419	CTCGACACGTGGCGACCGGTG	CGCGACGTGCGACGCCACTCGCTACCAATCTCCACACG	1478	
Db	750	GATCTCACACTAGAACAGACCT	CTATGTGATCCACATCTCTTACCCTCTCACC	809	
QY	1479	GACCACGTGGCGGCTTGGAGGTG	TGGCGGAGGGCGGTGGCGGCGCATCGGCGCTCGC	1538	
Db	810	GACCATGTTAATGGCTTCAAGT	CTTTTGGAAATCAATGGCGCTCAATGTCCTCCAC	869	
QY	1539	CCGGGCGCTCGTGGTCAACGTG	CGCGCACACTTCAATGGGCGCTCTCCACGCCAGTAC	1598	
Db	870	CCCAAGGCTTTGGTCAATATCGG	CGATACTTTCATGGCTCTATCGACAGATAGATAC	929	
QY	1599	CGCAGCTGGCTCACCGGGGGTGTG	CTCAACAGCAGCGGCGCTCGCGGCTCGTGGCTCC	1658	
Db	930	AAGAGCTGTTCACCGGGGSGTGTG	ATGACAGCGAGAGCGAGGAAATCACTTGCATTC	989	
QY	1659	TTCCTTGGCCGGAGTGGACAGTGTG	CGCCCGCGGAGGAGCTGTGTCAGACCCAC	1718	
Db	990	TTCCTTGGTCCGAAAAGACAGATG	ATGTGACGCCACCGAGAGAGCTTTTGGACAGCATC	1049	
QY	1719	CACCCGAGGGGTATCCCGGACTT	TCACGTGGCGGGCGCTGCTGGACTTCAGCAGGCGCAC	1778	
Db	1050	ACATCAGAGAGTACCCTGACTT	CCATGCTCATGCTGTATGTCTCTGAGTCTACTCAGAAACAT	1109	
QY	1779	TACAGGCGCACATCGCAGCGCT	TTCAGGCGCTTCCGACTGGCTTA	1824	
Db	1110	TATAGACAGACATGAACACTT	CCCAAGCGCTTTTCAGATTGGCTCA	1155	

RESULT 4

AAQ75361
ID AAQ75361 standard; cDNA to mRNA; 1490 BP.

XX
PN
WC9428741-A-

Db 814 GACCTATTGTGATCCAAAGTCTTTTGACCATCCCTTCAATCAAGACCAATGTCATATGCTTC 873
 QY 1498 AGGTGTGGGGGAGGGGGGGTGGCGCGCCATCCGCCCTCCCGGGGGGGTGGCGTTCGTCGA 1557
 Db 874 AAGTCTTTGTGCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 933
 QY 1558 AGTGGGGGACACCTTCATGCGGGCTCTCCACGCGCAGGTACCGCAGCTGCGTGGCACCGGG 1617
 Db 934 AATATGTGTGACACTTCATGCGCTCTATCGAAGCGGATATTCAGAGAGCTTTTGTGATAGAG 993
 QY 1618 CGGTCTCAACAGCAGCGGGCTCCCGCTCGTGGCTTTCTTCCTCTCCCGGGAGTGG 1677
 Db 994 CGTGTGATGATGAGAGCGGAGAAATGATGCGGCTTTTCTTGTCTCCGAGAAAG 1053
 QY 1678 ACACGGTGGTGGCGCGCGGGAGGCTGGTGCAGCAGCACCAACCGAGGGTGTACCGGG 1737
 Db 1054 ACAAGTGGTGAACACCAACCAAGTATTTTGGAGAGATGAAACAGAAATACCCCTG 1113
 QY 1738 ACTTCAGTGGGGGCGTGTGGTGTCTACGACAGCCCTACACAGGCGGACATGGCGCA 1797
 Db 1114 ACTTCAGTGGTGTATGTTCTTGTGATGTTCACTCAAAACATTACCGAGCAGATGTGAATA 1173
 QY 1798 CCGTTCAGGCGCTCTCCGACTGGCTTAAT 1826
 Db 1174 CTCCTGATCTCTTCTAATGGTAT 1202
 RESULT 5
 AAD21991
 ID AAD21991 standard; cDNA; 1420 BP.
 XX
 AC AAD21991;
 XX
 DT 12-FEB-2002 (first entry)
 XX
 DE Citrullus lanatus Cv20ox cDNA.
 XX
 KW Testa specific Cv20ox gene; gibberellin 20-oxidase; GA 20-oxidase;
 KW Cv20ox promoter; Cv20oxp; seedless fruit generation; watermelon;
 KW melon; ss.
 XX
 OS Citrullus lanatus.
 XX
 PH Key Location/Qualifiers
 FT CDS 70..1209
 FT /*tag= a
 FT /product= "C. lanatus GA 20-oxidase"
 XX
 PN WO200177310-A1.
 XX
 PD 18-OCT-2001.
 XX
 PF 09-OCT-2000; 2000WO-KR01127.
 XX
 PR 08-APR-2000; 2000KR-0018483.
 XX
 PA (DONG-) DONGBU HANNONG CHEM CO LTD.
 XX
 PI An G, Kang H, Jun S, Kim J, Jung K, Park Y, Lee S;
 XX
 DR WPI: 2002-010905/01.
 XX
 DR P-PSDB; AAE13273.
 XX
 PT Novel testa specific Cv20ox gene, a gibberellin 20-oxidase gene, which
 PT is integument-specifically expressed in seeds of Citrullus lanatus
 PT useful for producing seedless fruits such as melon
 XX
 PS Claim 2; Page 53-55; 59pp; English.
 XX
 CC The invention relates to testa specific Cv20ox gene, a gibberellin
 CC 20-oxidase (GA 20-oxidase) gene which is integument-specifically
 CC expressed in seeds of the Citrullus lanatus, and proteins encoded
 CC by such genes. The invention also relates to Cv20ox promoter

CC (Cv20oxp) which regulate the expression of Cv20ox gene and method
 CC for generating seedless fruits of gourd family such as melon or
 CC watermelon using the Cv20oxp sequence. The present sequence is
 CC C. lanatus Cv20ox cDNA coding for GA 20-oxidase.
 XX
 SQ Sequence 1420 BP; 412 A; 257 C; 329 G; 422 T; 0 other;

Query Match 9.2%; Score 229.6; DB 24; Length 1420;
 Best Local Similarity 55.3%; Pred. No. 3.7e-36;
 Matches 501; Conservative 0; Mismatches 384; Indels 21; Gaps 2;

QY 926 CCGGAGTGGGGAGGCGTGGAGAGGCGGCTTCTTCTCTGGTGGTAAACCGGAT 985
 Db 288 CAGGCTGGTGGTGAAGCGCTGTAGAAAACATGATCTTTGTGTGGTGAACCGGAT 347
 QY 986 CGAGGCGCGCTGTGGAGAGGCGCACCGGTGCATGAGCGCTTCTTCAACGCTGCGCT 1045
 Db 348 TGATATGAATGATAAAGGGGTTCTAGTGTATGGATGAGTTTTTTCACATTGCCCTT 407
 QY 1046 GGGGAGAAAGCAGCGGCGCAGCGGCGGAGAGCTGGGCTAGCGCAGCAGCTT 1105
 Db 408 TGATGTGAACAAAATCTCAAAGGAAATTTGGTGAATATATGGTATGCTATAGCTT 467
 QY 1106 CAGGGGCGCTTGGCTCCAGTCCCGTGGAGAGAGCGCTGTCTCCGCTACTATC 1165
 Db 468 CATTTGGAAGATTTCCCAATAATCTTCCATGGAAGAAACCTTTCCCTTC----- 517
 QY 1166 GGCTGGAGATGAAGAGGCGGAGAGGCGGTGGTGAATCTGCTGCGGAAGCTCGGGC 1225
 Db 518 --CTTATGTGCTAAATCAATAATTCACCTCTGTTCAAGATTTCTGTTTAAATGTTGG 575
 QY 1226 GGAGCAGCGGCGGCGTGGGAGGTGTACTCGCTACTGCGCAGAGATGAGCGGCT 1285
 Db 576 CCCAGATTTATCCATCAAGGAGGTGTATCAAGATTTGGAAGAGATTGAGTGATCT 635
 QY 1286 GTGCTGGAGCTGATGGAGTGTCTGGGAGAGCTGGGCTGCTCGGAGAGCGGCGCA 1345
 Db 636 GAGTTTGAAGATGATGGAGCTATTTGGGTTGAGCTAGGGTTTCCAAAAG-----A 686
 QY 1346 CTACTTCCGGGATTCTTCCAGCGCAAGACTTCCATCATGCGCTCAACTACTACCGCGC 1405
 Db 687 GAAGTTCAAAAATCTATGAGGACATGATCAATTAAGCTGAATTAATACCACC 746
 QY 1406 GTGCCAGAGGCGCTGACACAGCTGGGACCGGCTCCGCACTCGGACCCCACTGCTCAC 1465
 Db 747 ATGCGAAGAGCGCAGAGCTGACATTTGGAACTGGGCTCACTGTGATCCCAACCTCATAAC 806
 QY 1466 CATCTCCACAGCAGCAGCTCGGCGGCTGGAGTGTGGGCGGAGGCGGTGGCGGC 1525
 Db 807 AATTCTTCACAGACCACTCAGTGGCTTCAAGTCTAGTGTATGATGATGAGTGCATC 866
 QY 1526 CATCGCGCTCGCCCGGGCGCTGTCTCAAGTCTGGGACACCTTCAATGCGCTCTC 1585
 Db 867 AATTCTTCACAGCAAGGACTCTCTTTGATCAATATCGGTGACACTTTTCAATGCTGAC 926
 QY 1586 CAAACCCAGGTACCGCAGCTGCTGACCGGGGCGTGTCAACAGCAGCGGCGCTCGCGG 1645
 Db 927 AATAGGGGTTTACAAGAGCTGTCTCCACCGAGCTGTAGTGAAGTGAAGAA 986
 QY 1646 CTCGTGGCGCTTCTTCTCTGCGGAGATGACACGCTGTGGCGCGCGGAGAGCT 1705
 Db 987 ATCAATGCGCTTCTTCTATGTTCCAGCGGCTGACAAAGTGTGAGAGCAGCGAGAGT 1046
 QY 1706 GGTGAGCAACCAACCGGAGGTGTACCCGAGTTCACGTGGGCGGCGCTGCTGGAATT 1765
 Db 1047 GGTGAGAGAAATCCCAAGGAAGTTTCCAGATTACATGATGCAATGCTCTTGAAGT 1106
 QY 1766 CAGCAGCGCCACTACAGGCGCAGATGCGGACGCTTCAGGCTTCTCGACTGCTTAA 1825
 Db 1107 TACCAAAAATTTTATAGGCTGATTCACAGACTTTTACAGGCGCTTCACTCTGCTGA 1166
 QY 1826 TCATCA 1831
 ||


```
Db 1167 AAARCA 1172
RESULT 6
AAQ75359
ID AAQ75359 standard; cDNA to mRNA; 1395 BP.
XX AC
XX AAQ75359;
XX 01-JUL-1995 (first entry)
XX DE
XX Gibberellin-20-oxidase.
XX KW Gibberellin-20-oxidase; plasmid pB11; transgenic plant;
XX KW crop improvement; ss.
XX OS
XX Cucurbita maxima.
XX PH Key Location/Qualifiers
XX FT 15..1341
XX FT /*tag= a
XX FT /note= "GA-20-oxidase"
XX PN
XX W09428141-A.
XX PD
XX 08-DEC-1994.
XX PF 24-MAY-1994; 94WO-EF01664.
XX PR 28-MAY-1993; 93GB-0011147.
XX PA (LONG-) LONG ASHTON RES STATION.
XX PI Graebe JE, Hedden P, Lange T, Phillips A;
XX WPI; 1995-022813/03.
XX DR P-PSDB; AAR67450.
XX CC
XX PT New DNA encoding gibberellin 20-oxidase and related vectors -
XX PT also host cells and transgenic plants, used to modulate plant
XX PT growth and development, e.g. anti:sense constructs will reduce
XX PT vegetative growth.
XX PS Claim 8; Page 72-73; 97pp; English.
XX CC Vectors containing DNA encoding gibberellin-20-oxidase activity are
XX CC used to construct chimeric genes and binary vectors to transform
XX CC plants by usual methods, e.g. Agrobacterium-mediated transfer.
XX CC Propagated transgenic plants show modulated growth and development
XX CC e.g. reducing GA-20-oxidase expression with antisense constructs
XX CC reduces vegetative growth in cereals and grasses, improving
XX CC resistance to frost, etc. Sense constructs improve fruit set and
XX CC growth, extended stems and leaves, induce flowering and overcome
XX CC dormancy, etc. Preferred transgenic plants are maize and wheat.
XX SQ Sequence 1395 BP; 404 A; 288 C; 336 G; 367 T; 0 other;
Query Match 9.1%; Score 228; DB 16; Length 1395;
Best Local Similarity 55.3%; Pred. No. 7.6e-36;
Matches 497; Conservative 0; Mismatches 380; Indels 21; Gaps 2;
QY 928 GGCAGGTGGGGAGCGTGGAGAGGACACGGCTCTTCCTGGTGGTAAACACGCGCATCG 987
DB 247 GCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 306
QY 988 AGCGCGCGTGGTGGAGAGGCGCAGCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1047
DB 307 ACATAGAATATGGCGCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 366
QY 1048 GGSAGAGAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGTCA 1107
DB 367 ATGTGAAGCAGAGGCGCTAAGAGGCGAGGTAGGTAGGTAGGTATGATATACCATAGCTCT 426
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QY 1108 CGGGCGCTTGGCTCCAAAGCTCCGCTGGAGAGAGAGCTGTCTCCGCTACTCAATCGG 1167
DB 427 TTGGAGATTGGCTCCAAATCTTCCATGAAGAAACCTTTCCCTTCGCTGTGTGGCTG 486
QY 1168 CTGGAGATGAAGAGGCGGAGAGGCGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1227
DB 487 CTCAAACTCTCCGCGGCTCATGACTATGTCTTGTGACATTTAGGCCCATCATTTCTCC 546
QY 1228 AGCAGCGGCGGCGGTGGGAGGTGTACTCGCGTACTCCACAGATGAGCGCGCTGT 1287
DB 547 ATCATGGG-----AAGCGTATCAGAGTGTGGGATAGCATTTGACGAGCTTG 594
QY 1288 CGGTGAGCTGATGAGGTGCTCGGGAGAGAGCGTGGGAGATGCTGGAGACCGGCCACT 1347
DB 595 GTACGAAGATTGTGAGCTTTTGGGCTTAGCTTTGGCAATTTCAAGAG-----AAT 645
QY 1348 ACTTCGGCGATTTCTTCAGCGCAAGACTCCATCATCGGCTCAACTACTACCGGGGT 1407
DB 646 ACTTCAAGANTTCTTCGAGGACACAGTTCATATTTAGAGCTTAATTACTACCAACAT 705
QY 1408 GCGAGAGGCGCTGACACAGCTGGGACCGGCTCCGCTCCGCTGCGACCCACCTCGCTCACA 1467
DB 706 GCGACAAGCCAGAGGTGTGTGGAACTGGCCCTCACACTGATCCCACTCCGCTCAAA 765
QY 1468 TCCTCCACAGGACACAGCTGGGCGCTGAGGTGTGGGCGGAGGCGGTGGCGGCGCA 1527
DB 766 TCCTTCCCAAGACCTGTGAGTGGCTTCAAGTGTGCTCCATGATCAATGATGATCAA 825
QY 1528 TCCGCGCTCGCCCGGGGCGTGTGTCAAGCTGGGAGACACCTTCATGCGGCTCTCCA 1587
DB 826 TTCTCTCAAAACCCAGAGCTTTGTATCATACATCGGTGACACTTTCACGTCTCTCAAGA 885
QY 1588 ACGCCAGGTACCGAGCTGCTGCGACCGGCGGTGCTCAACAGACGCGGCTTCGCGCT 1647
DB 886 ATGGGATTTCAGAGGCTGCATACCGCGCTGTAGTGAATTCCTGATGATGAGAGAAAT 945
QY 1648 CGCTGGCTCTTCTTCCTGCGCGGAGATGACACGCTGTGGTGGCGCGCGGAGAGCTGG 1707
DB 946 CATGGCTCTTCTTCTGTGCTCATGACAAAGTGTGAGAGACACCGGAGATTTGG 1005
QY 1708 TCGACGACACACCGGAGGTGTACCGGACTTCACGTGGCGGCGCTCTCGGACTTCA 1767
DB 1006 TGGAGAAGAGTCCACACGAAAGTATCCAGATTATATAATGGCCAATTTGCTTGAATGA 1065
QY 1768 CGCAGCGCTACAGGCGCGACATGCGCAGCTTCAGCGCTTCCGACTGGCTTAA 1825
DB 1066 CCAAAAGGTTACCGACTGATTCGACACTTTGGAAGCTTCAAACTTGGGTCA 1123
RESULT 7
AAZ99483
ID AAZ99483 standard; cDNA; 1161 BP.
XX AC
XX AAZ99483;
XX DT 03-JUL-2000 (first entry)
XX DE cDNA encoding a C-20 oxidase polypeptide.
XX KW Gibberellic acid; copalyl diphosphate synthase; 3beta-hydroxylase;
XX KW 2-oxidase; phytoene synthase; C-20 oxidase; 2beta,3beta-hydroxylase;
XX KW seed germination; seedling growth; gibberellin biosynthetic pathway;
XX KW transgenic plant; hypocotyl; epicotyl; ss.
XX OS Cucurbita maxima.
XX FH Key Location/Qualifiers
XX FT 1..1161
XX FT /*tag= a
XX FT /product= "C-20 oxidase"
XX PN W0200009722-A2.
XX
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QY	803	GCAGACGAGATCCCGTCGCAGTTTCATATGCCCGCGGAGGAGAGCCCCGGTCTGGTGGC	862
Db	126		
QY	863	GCTGGAGAGAGTGGAGTGGCGCTGATCGAGCTGGCGCGCGGGGGGAGAGGTGCTGGT	922
Db	186		
QY	923	GGACCCCTTCTGGACCTAGCAATCTTTAAAGATGTTGACGAGAAAGCTATTTCCAATGC	245
Db	923		
QY	246	AGCAGAGCTTGTGAGAAAGCATGCTTGAAGCATGGTCTTTTCCAAAGTGATAAACCATTGG	305
Db	983		
QY	306	CATCGAGCGCGCTGCTGGAGAGGCGACCGGTGCATCGAGCGCTTCTTCACGCTGCC	1042
Db	1043		
QY	366	TGTGGACCCAGATCTATTGATGCTGCATATCATGAATTGACTCCATTTTATAGCTCCC	365
Db	1102		
QY	426	CTCATCGAGATCGTTATTTGTCCTCAAGTTCGCATGAAGAGACGTTTCTTCTCTA--	483
Db	1162		
QY	484	-----TGATCACCAGAAGCTTCCACTCCAGATTGTTGACTACTTCAAGTCTGTT	536
Db	1222		
QY	537	TAGGGGAGGATCTTCAACACACAGAGGAGGTATACAAAGTACTCGGAGGCAATGAAGG	596
Db	1282		
QY	597	ATTTATCTTTAGTAAATTAAGGACTATTGGTATATTGKTTG-----GGTGGGATC	648
Db	1342		
QY	649	GTGAGCATTATCGAAGATTTTTTCAAGATGGTGACTCAATAATGAGGTGCAACTATTATC	708
Db	1402		
QY	709	CACCTTGAACAGAGCGAACCCTACCTTAGGCATCGCCCTCACCTGATGATCAACCTCAC	768
Db	1462		
QY	769	TACCATCTCTCCACAGGACCGTTCGCGCGCTGAGAGTGTGGCGGAGGGCGGTGGC	1521
Db	1522		
QY	829	TGCGTGTTCGCCCTTCGATCTGAAGCCTTAGTCAATAAATAGGTGATATCTTCATGGCAT	888
Db	1582		
QY	889	TCTCCAAGCCAGGTACCGAGTCCCTCGACCGCGCGGTCTCTACACAGCGCGCCTC	1641
Db	1642		
QY	949	GAAGTCCCTTGTTATTTTGTGTGTCACAGAGGACCAATAGTGTAGNCCCCAGACA	1008
Db	1702		
QY	1009	ATTTGTTATGCAAAATAGAGAAAGAGTACCTCTGATT	1047
Db			

RESULT 10
AAZ99478
ID AAZ99478 standard; CDNA; 811 BP.
XX
XX AAZ99478;
XX AC
XX AC
DT 03-JUL-2000 (first entry)

XX	Maize gibberellic acid 2-oxidase 2 cDNA sequence.
XX	
XX	Gibberellic acid; copalyl diphosphate synthase; 3beta-hydroxylase;
KW	2-oxidase; phytoene synthase; C-20 oxidase; 2beta,3beta-hydroxylase;
KW	seed germination; seedling growth; gibberellin biosynthetic pathway;
KW	transgenic plant; hypocotyl; epicotyl; ss.
OS	Zea mays.
XX	
PN	WO200009722-A2.
XX	
PD	24-FEB-2000.
XX	
PF	10-AUG-1999; 99WO-US18066.
XX	
XX	10-AUG-1998; 98US-0096111.
PR	07-JUN-1999; 99US-0137977.
XX	
PA	(MONS) MONSANTO CO.
XX	
PI	Brown SM, Eich TD, Heck GR, Kishore GM, Logusch EW, Logusch SJ;
PI	Piller KJ, Rao S, Ream JE;
XX	
XX	WPI; 2000-224351/19.
PT	Obtaining transgenic plant useful for controlling seed germination and
PT	seedling growth comprises transgene comprising a sequence expressing
PT	altered levels of an essential hormone
XX	
PS	Claim 45; Page 253; 267pp; English.
XX	
CC	The present sequence represent a gibberellic acid 2-oxidase 2 cDNA
CC	sequence, which is used in the method of the invention. The specification
CC	describes methods for the inhibition and control of gibberellic acid
CC	levels. Gibberellic acid levels may be inhibited or controlled by use of
CC	a chimeric expression construct expressing a RNA or protein which
CC	suppresses the gibberellin biosynthetic pathway sequence, diverts
CC	substrate from the pathway, or degrades pathway substrates or products.
CC	The methods uses copalyl diphosphate synthase, 3beta-hydroxylase,
CC	2-oxidase, phytoene synthase, C-20 oxidase, and a 2beta,3beta-hydroxylase
CC	polynucleotides to achieve this. The method is used to control seed
CC	germination and seedling growth especially to regulate gene products of
CC	gibberellin biosynthetic pathway and restoration of normal seed
CC	germination, in transgenic plants. The plants produced are gibberellin
CC	deficient, and have shortened hypocotyl and/or epicotyl phenotypes
CC	compared to normal plants.
XX	
SQ	Sequence 811 BP; 134 A; 249 C; 278 G; 150 T; 0 other;

Query Match	5.2%;	Score 129;	DB 21;	Length 811;
Best Local Similarity	56.9%;	Pred. No. 3.1e-16;		
Matches 278;	Conservative	0;	Mismatches 205;	Indels 6; Gaps 2
QY 1274	GATGAGCCGCTGTGCTGGAGCTGATGGAGGTGCTCGGGGAGAGGCTGGGCATCTGCGG	1333		
Db 22	GATGCGGTGCGCGGTGTGGAGTGTATGCGGAGGGGCTGGGCATCGCGGGCGGCGCGG	81		
QY 1334	AGACGGCGGCACCTACTTCGCGGCGATTCTCCAGCAACGACTCCATCATGCGGCTCAA	1393		
Db 82	GGACCGGTGTGTGGCGGGGTGGTGGCGCGCGCGAGCAGCGACTGATGCTGCGGGTGAA	141		
QY 1394	CTACTACCGGCGCTGCCAGAGGCCACTCGACACGCT---GGGCACCGGTTCGCSACTCGGA	1450		
Db 142	CCACTACCGCGCGCGCGGCGCTCAACCCAGCGCTCACGGGGTTTCGGGAGCACACCGA	201		
QY 1451	CCCCACTCTGCTTACCATCTCTCCACAGGACCAAGTCGGCGGCGCTGGAG---GGTGGGC	1507		
Db 202	CCCGAGATCATCTGGGTGTCTCGCGGCCAACGGCACCTCGCGCTGGAGATCGCGCTGG	261		
QY 1508	GGAGGGGCGGTGGCGGCCATCGGCCCTTCGCCCGGGGCGCTCGTGTCAAGCTCGGCGA	1567		
Db 262	GGAGGGGCGCTTGGGCTCTCGTCCCGCGAGGGAGGCGCTTCTTGTTCAAGCTCGCGA	321		

CC encoding the stabilising polypeptide can be linked onto or inserted into
CC a nucleic acid encoding a core protein. The fusion proteins of the
CC invention are more resistant to degradation by proteases and, thus, have
CC a longer half-life than the unfused core protein. The products can be
CC used for treating autoimmune diseases, cancer and inflammation. In
CC particular, the core protein may be an IkappaB regulator protein for the
CC treatment of inflammatory bowel disease, or a nitroreductase protein
CC which can activate nitro drugs in enzyme/prodrug therapy to treat cancer
CC or other pathological conditions. The fusion proteins can also be used in
CC diagnostic methods such as in vivo imaging.

XX Sequence 799 BP; 201 A; 106 C; 479 G; 13 T; 0 other;

Query Match 3.8%; Score 94.4; DB 19; Length 799;
Best Local Similarity 49.2%; Pred. No. 2.3e-09;
Matches 248; Conservative 0; Mismatches 256; Indels 0; Gaps 0;

QY 752 GGTGTCACGAGGAGGCGTGTTCGACGGCGGCTGTGAGCGGGCAGACGCA 811
DB 68 GGACAGAGAGGGGCGACGAGGAGGAGGGGCGACGAGGAGGGCGAGGAGG 127
QY 812 GATCCCGTCGACATATATGCGCGGCGAGAGAGCCCGGGTCTGCGGTGAGGA 871
DB 128 GCAGGACGAGAGGGGCGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 187
QY 872 CTGAGGTCGCTGATCGACGTGGGGCGGGGCGGAGAGGTCGTCGTCGTCGCGCA 931
DB 188 CAGGAGAGGGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 247
QY 932 GGTGGGAGGCGTCGAGAGGCGACGCTTCTTCCTGTGTGTTTACACGCGATCGAGG 991
DB 248 GGAGGGCGAGGAGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 307
QY 992 GCGCTCTGAGGAGGCGACCGCTGATGACGCTTCTTCAGCTGCTGCTGCGTGGGGA 1051
DB 308 CAGGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 367
QY 1052 GAAGCAGCGGCGACGCGCGGCGGAGGAGCTGCGCTACGCCAGCAGCTTCACGGG 1111
DB 368 CAGAGGGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 427
QY 1112 GCGCTTCGCTCAGCTGCGCGTGAAGGAGAGCGCTGCTGTCGTCGTCATCCTGCG 1171
DB 428 CAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 487
QY 1172 AGATGAGAGGCGAGGAGGCGCTGGTGTGATCTACTGTCGCGAGCTCGGGCGGAGCA 1231
DB 488 GGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 547
QY 1232 CCGGCGGCGCTGGGCGAGGTGTA 1255
DB 548 GGAGGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 571

RESULT 14

AAA50254

ID AAA50254 standard; DNA; 1926 BP.

XX AAA50254;

XX AAA50254;

DT 07-NOV-2000 (first entry)

DE Epstein Barr virus nuclear antigen 1 protein (EBNA1) DNA.

XX EBV; nuclear antigen 1; EBNA1; episome; transfection; selection;
KW gene therapy; ds.

OS Epstein-barr virus.

XX WO200047778-A1.

XX 17-AUG-2000.

PF 11-FEB-2000; 2000WO-US03547.
XX 11-FEB-1999; 99US-0249585.
XX (PHAR-) PHARMACOPETIA INC.
XX Horlick RA, Chelsky D;
XX WPI; 2000-515062/46.
XX P-PSDB; AA95856.
PT Stably transfecting eukaryotic cells with at least one episome for the
XX production of a desired protein in vitro and for gene therapy -
XX Disclosure; Fig 2; 53pp; English.

CC The present sequence is that of DNA encoding the Epstein-Barr virus
CC (EBV) nuclear antigen protein 1 (EBNA1, see AA95856). EBNA1 is
CC utilised in a novel method for obtaining a eukaryotic cell that is
CC stably transfected with at least one episome. This method involves
CC transfecting a eukaryotic cell with: (1) a first episome comprising
CC an EBV origin of replication (oriP, see AAA50253), a gene encoding a
CC first protein whose expression results in cell death and a
CC selectable marker for eukaryotic cells; and (2) a second episome
CC comprising an EBV oriP and a gene encoding a second protein, where
CC expression of the second protein prohibits the occurrence of cell
CC death resulting from expression of the first protein to produce
CC doubly transfected cells which also express an antigen that
CC promotes retention of the episomes by the cells. The doubly
CC transfected cells are maintained under conditions in which the
CC first and second proteins and the selectable marker are expressed,
CC and the selective pressure specified by the marker is maintained.
CC Under these conditions, only cells containing both episomes live.
CC Preferably, EBNA1 is expressed from 1 of the episomes, and the
CC protein of interest from the other episome. Either or both
CC epitopes may further comprise a nucleic acid sequence encoding a
CC protein desired to be expressed in the cell (e.g. a therapeutic
CC protein), a nucleic acid encoding an RNA that is not intended to
CC be translated (e.g. a therapeutic RNA), or a DNA sequence used as
CC a tag for the cells. The method is applicable to cell culture or
CC intact organisms, for gene therapy. It allows the rapid
CC establishment of eukaryotic cells that stably and reliably express
CC a gene of interest, using a novel method of selection, and
CC maintenance of that selection without the need for exogenous
CC selection factors, such as antibiotics.

XX Sequence 1926 BP; 487 A; 352 C; 872 G; 215 T; 0 other;

Query Match 3.8%; Score 94.4; DB 21; Length 1926;
Best Local Similarity 49.2%; Pred. No. 2.9e-09;
Matches 248; Conservative 0; Mismatches 256; Indels 0; Gaps 0;

QY 752 GGTGTCGACGAGGAGGAGGCTGTTCGACGGCGGCTGTGAGCGGGCAGACGCA 811
DB 310 GGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 369
QY 812 GATCCCGTCGACATATATGCGCGGCGAGGAGAGCCCGGGTCTGCGGTGAGGA 871
DB 370 GCAGGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 429
QY 872 GCTGAGAGTGGCGCTGATCGACGTGGGGCGGGGCGGAGAGGTCGTCGTCGTCGCGCA 931
DB 430 GCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 489
QY 932 GGTGGGGGAGGCGTCGAGAGGCGACGCTTCTTCTGTGTGTTTACACGCGCATCGAGC 991
DB 490 GGAGGGGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 549
QY 992 GGGCGCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1051
DB 550 GCAGGAGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 609
QY 1052 GAAGCAGCGGCGCAGCGCGCGCGGGGAGAGCTGCGGCTACGCCAGCAGCTTCAGCGG 1111

Db	610	GCAGAGGGGCAGAGGGGCAGAGGGGCAGAGAGGGGCAGAGAGGAGGAGG	669
QY	1112	GGGCTTCGCTCCAAAGCTGCCCTGGAAGACAGCTGTGTTCCGGTACTCATCGGTGG	1171
Db	670	GCAGAGGGGCAGAGGGGCAGAGGCACGAGCGGGGCAGAGAGGGGCAGGACAGGA	729
QY	1172	AGATCAGAGGGGCAGAGGGGCTGGGTAGTACTCTGGTCGGAAGCTCGGGGCGGAGCA	1231
Db	730	GGGGCAGGACAGAGGGGCAGAGGGGCAGAGAGGGGCAGAGAGGGGCAGGAGCA	789
QY	1232	CGGGGCGGCTGGCGAGGTGTA	1255
Db	790	GGAGGGGCAGAGGGGCAGGAGCA	813

RESULT 15	
AAAF82902	
ID	AAAF82902 standard; DNA; 1936 BP.
XX	
XX	
AC	
AC	
XX	AAAF82902;
XX	
DT	29-JUN-2001 (first entry)
XX	
XX	
DE	EBV tethering protein EBNA1 encoding DNA.
XX	
XX	
KW	Histone H1; tethering protein; LANA; gene therapy; multiple sclerosis;
KW	Parkinson's disease; Huntington disease; diabetes; human herpesvirus 8;
KW	EBV; latency-associated nuclear antigen; LANA; EBNA1; GS.
XX	
XX	
OS	Epstein-barr virus.

PH	Key	Location/Qualifiers
FI	CDS	i..1926
FI		/*tag= a
XX		
XX		WO200125484-A2.
PN		
XX		
PD		12-APR-2001.
XX		
PF		29-SEP-2000; 2000WO-US26908.
XX		
PR		01-OCT-1999; 99US-0410399.
XX		
PA	(UNMI) UNIV MICHIGAN.	
XX		
PI	Robertson ES, Cotter MA;	
XX		
XX	WPI; 2001-281736/29.	
DR	P-PSDB; AAB62332.	
DR		

XX A composition for use in gene therapy comprises an expression vector
PT that includes a nucleic acid sequence encoding a nucleic acid binding
PT protein -
XX
PS Disclosure; Fig 9C; 60pp; English.

The invention provides a composition comprising nucleic acid, histone H1 protein and expression vector operationally encoding a protein suitable for tethering the nucleic acid to the histone H1 protein, where the tethering protein is IANA. The composition is useful in aiding the retention of the viral DNA in the host cell. The viral vector encodes a protein suitable for tethering DNA to histone H1. Methods for screening for compounds which are agonistic or antagonistic for the tethering of viral proteins to histone H1 and DNA binding sites are useful for developing the method of viral transfer. The composition has applications to gene therapy, including the treatment of multiple sclerosis, Parkinson's disease, Huntington disease and diabetes. The present sequence represents the nucleotide sequence of the Epstein-Barr virus (EBV) tethering protein ENNA1.

Sequence 1926 BP; 487 A; 352 C; 872 G; 215 T; 0 other;

Query Match	3.8%;	Score 94.4;	DB 22;	Length 1926;	
Best Local Similarity	49.2%;	Prod. No. 2.9e-09;			
Matches 248;	Conservative	0;	Mismatches 256;	Indels 0;	Gaps
QY	752	GTGCGTGCAGCAGGACAGAGAGTGGTTCGACCGCGCGGTCTCGAGCGGCGACACGGA	811		
Db	310	GGAGCAGGAGGAGGGCAGGACAGAGAGAGGCGAGGCGCAGAGGGCGACAGGGCGACGAGGG	369		
QY	812	GATCCCGTCGACGTTTCATATGCGCGCGAGAGAGCCCGCGTCTCGGTGGCGGTGGAGGA	871		
Db	370	GCAGGAGCAGGAGGAGGGCGCAGGACGAGGAGGGCGCAGAGGGCGAGGGCGAGGA	429		
QY	872	GCTGAGGTGCGCTGATGACGTGGGGGGCGGGCGGAGAGTCTCGTGGTGCOCGGCA	931		
Db	430	GCAGGAGGAGGGCGAGGACGAGGAGGAGGGCGCAGGAGGCGCAGGAGCAGGAGGAGGGCGA	489		
QY	932	GGTGGGGGAGCGTCCGAGAGGCGACGGCTTCTTCTGGTGGTTAACCCAGCGCATCGAGGC	991		
Db	490	GGAGGGGCGAGGAGGGCGAGGACGAGGAGGAGGGCGCAGGAGGAGGGCGACGAGGGCGAGGAGG	549		
QY	992	GCGGTGCTCGAGGAGGCGCACCGGTGATGGACGCGCTTCTTCACTGCCCTGGGCGGA	1051		
Db	550	GCAGGAGCAGGAGGAGGGCGCAGGAGGGCGCAGGAGGCGCAGGAGGAGGGCGAGGA	609		
QY	1052	GAAGCAGCGGGCGCAGCGCGCGCGGGGGAGAGTTCGGGCTACGCCACAGCTTCAOCGGG	1111		
Db	610	GCAGGAGGGCGCAGGAGGGCGAGGAGGGCGCAGGAGGAGGGCGCAGGAGGAGGAGGG	669		
QY	1112	GCGCTTCGCTCCAGCTGCCGTGGAGAGAGACGCTCTCTTCCGCTATCTCATCGGTGG	1171		
Db	670	GCAGGAGGGCGCAGGAGGGCGAGGACGAGGAGGGGCGAGGACAGGAGGGCGAGGAGGGCGAGGAGGAGGA	729		
QY	1172	AGATGAGAGGGCGCAGGAGGGCGTGGGTGAGTCACTGGTGGCGAACTCGGGGCGGAGCA	1231		
Db	730	GGGGCAGGAGCAGGAGGGCGCAGGAGGGCGCAGGAGGGCGCAGGAGGGCGAGGAGGGCGAGGAGCA	789		
QY	1232	CGGGCGGCGGCTGGGCGAGGTGTA	1255		
Db	790	GGAGGGCGCAGGAGGGCGAGGAGCA	813		

Search completed: March 26, 2003, 05:14:43
Job time : 417.887 secs

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OM nucleic - nucleic search, using sw model

Run on: March 25, 2003, 19:50:00 ; Search time 2548.43 Seconds
(without alignments)
15894.084 Million cell updates/sec

Title: US-09-702-134-7212_COPY_28000_30500

Perfect score: 2501

Sequence: 1 atgcgaagaataaattggc.....ctatcaatggttgcttaac 2501

Scoring table: IDENTITY_NUC
Gap 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estma:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	629.4	25.2	1435	11 AY105651	AY105651 Zea mays
2	286.8	11.5	536	12 BG322884	BG322884 EML_15.C1
3	277.4	11.1	755	12 BG365195	BG365195 HVSME1000
4	263.4	10.5	752	12 BG365194	BG365194 HVSME1000
5	261.4	10.5	796	12 BG299451	BG299451 HVSMEa002
6	255.4	10.2	577	10 BE194605	BE194605 HVSMEa008

7	230.4	9.2	914	12	BF620505	BF620505 HVSMEC002
8	213	8.5	682	12	BG416635	BG416635 HVSMEK001
9	209.8	8.4	566	12	BG414208	BG414208 HVSMEK000
10	203.8	8.1	571	10	BE454826	BE454826 HVSMEH009
11	200	8.0	567	14	BG608563	BG608563 BRY_2428
12	196.8	7.9	655	12	BG350197	BG350197 084C04_Ma
13	191.2	7.6	517	10	BE422495	BE422495 WHE0056_E
14	187	7.5	686	10	BE414214	BE414214 SCU007_E0
15	185.6	7.4	700	14	B0402912	B0402912 GA_Ed005
16	173.6	6.9	757	10	BR055752	BR055752 GA_Ea000
17	170.8	6.8	588	10	BE429459	BE429459 TAS000_D0
18	167.8	6.7	483	13	BI950763	BI950763 HVSMEI002
19	158.6	6.3	801	12	BG369047	BG369047 HVSMEI002
20	156	6.2	1084	11	AY108935	AY108935 Zea mays
21	151	6.0	612	14	BQ806836	BQ806836 WHE3583_G
22	142.8	5.7	472	17	AQ914586	AQ914586 nbe0049A
23	142.2	5.7	438	14	B0167179	B0167179 WHE0056_E
24	141.6	5.7	564	10	AW471536	AW471536 s113b09_Y
25	140.6	5.6	383	13	BI131287	BI131287 G118P39Y
26	140	5.6	350	10	BE500119	BE500119 WHE0978_D
27	138.6	5.5	513	9	AL506369	AL506369 AL506369
28	135.4	5.4	773	14	BQ743979	BQ743979 WHE4110_D
29	134.8	5.4	405	10	BE556197	BE556197 sp98g04_Y
30	134.4	5.4	675	14	B0402913	B0402913 GA_Ed005
31	133.6	5.3	590	10	AV563665	AV563665 AV563665
32	133.6	5.3	662	12	BE918296	BE918296 OVL_1_F10
33	130.8	5.2	412	12	BF293852	BF293852 WHE2153_G
34	130.6	5.2	583	10	AV560858	AV560858 AV560858
35	130.4	5.2	521	12	BE918082	BE918082 OVL_1_F10
36	130.2	5.2	761	14	B0807183	B0807183 WHE3587_G
37	130	5.2	666	14	B0413073	B0413073 GA_Ed006
38	129.8	5.2	803	10	AW48262	AW48262 BRY_1527
39	129.8	5.2	803	14	BG605936	BG605936 BRY_1527
40	128.6	5.1	1382	11	AY104706	AY104706 Zea mays
41	128.4	5.1	364	13	BI124052	BI124052 I035P04P
42	128.4	5.1	628	9	AL504453	AL504453 AL504453
43	127	5.1	665	14	B0415927	B0415927 GA_Ed010
44	126.6	5.1	472	10	B8403224	B8403224 WHE0426_H
45	126.4	5.1	479	13	BM136125	BM136125 WHE2605_A

ALIGNMENTS

RESULT 1	AY105651	AY105651	1435 bp	mRNA	linear	HFC 25-MAY-2002
LOCUS	Zea mays PC0130567 mRNA sequence.					
DEFINITION	Zea mays PC0130567 mRNA sequence.					
ACCESSION	AY105651					
VERSION	AY105651.1 GI:21208729					
KEYWORDS	HFC.					
SOURCE	Zea mays.					
ORGANISM	Zea mays					
REFERENCE	1 (bases 1 to 1435)					
AUTHORS	Rukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.					
TITLE	Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes					
JOURNAL	Unpublished (2002)					
REFERENCE	2 (bases 1 to 1435)					
AUTHORS	Coe,E.C.					
TITLE	Direct Submission					
JOURNAL	Submitted (25-APR-2002) Maize Mapping Project, University of Missouri, Columbia, MO 65211, USA					
FEATURES	Location/Qualifiers					
SOURCE	1..1435					
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	/clone="PC0130567"					

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/clone_lib="Maize Mapping Project/DuPont Consensus
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/notes="this sequence is part of a project of EST
assemblies resulting from the application of public
contigs to seed Dupont contigs; this resource was
assembled by Dupont as part of a collaboration for the
overgo addressing of BACs in conjunction with the Maize
Mapping Project"
BASE COUNT      284 a  461 c  427 g  263 t
ORIGIN
Query Match      25.2%; Score 629.4; DB 11; Length 1435;
Best Local Similarity 75.9%; Pred. NO. 1.1e-118;
Matches 825; Conservative 0; Mismatches 241; Indels 21; Gaps 3;

QY 744 ATGACATGTTGGTTCAGCAGGAGGAGGTGTTTCAGCGGGGTGCTGAGCGGG 803
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Db 67 ATGGTCTGGTGGCGACAGTCCCTCCCTTGTGTCGACGCTGCCCGCTGAGCGGC 126

QY 804 CAGACGAGATCCCGTCCAGTTTCATATGCGCGCGGAGAGAGCCCGGCTGGCG 863
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 127 CTCTCGCATCCCGACAGTTTCATCTGCGCGGCGAGAGAGCCCGCGGACTCC 186

QY 864 GTGGAGAGCTGGAGGTGGCGTTCATCAGTGTGGGGGGGGGGGGAGAGTCTCG 923
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Db 187 GCGAGAGAGCTGGCGGCTGCGCGCTCATCGACCTCTCCGGGGAGCGCG-----CCGAGGTG 240

QY 924 GTCCGCGAGGTGGGGAGGCGTGGCGAGGACAGCGCTTCTTCTGTTTAAACACGCG 983
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Db 241 GTCCGCGAGGTCCGCGCGCTCGACCTGTCACGCTTCTTCAGTGTGGGGACAGCG 300

QY 984 ATCGAGGCGGCTGCTGGAGAGGCGCCACCGGTGCATGAGAGCGCTTCTTCAGTGGCG 1043
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Db 301 ATCGAGGCGGCTGAGCGGAGGCGCCACCGCTGCATGAGAGCGCTTCTTCAGTGGCG 360

QY 1044 CTGGGGAGAGCAGCGGCGAGCGCGCGCGGGGAGAGCTGCGCTACGCCAGCAGC 1103
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Db 361 CTCCGCGACAGCAGCGCGCGAGCGCGCGCGCGCGAGAGCTGCGCTACGCCAGCAGC 420

QY 1104 TTCACGGGCGCTTCGCGTCCAAAGTTCGCGTGAAGAGAGAGCGTGTCTGCGGTACTCA 1163
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Db 421 TTCACGGGCGCTTCGCGTCCAAAGTTCGCGTGAAGAGAGAGCGTGTCTGCGGTACTCAC 480

QY 1164 TCGCTGAGATGAGAGGCGAGAGGCGTGGGTGATCTACCTGTCGAGAGTGGCG 1223
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Db 481 GAGCAGCAGCAGCGCGCAAGTCAAGAGAGAGCTGCTGCTCTTCTGTCGAGAGCTG 540

QY 1224 GCGGAGCAGCGCGCGCTGGCGAGGTGTACTCGCGCTACTGCCACGAGATGAGCGCG 1283
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Db 541 GCGGAGGCTACCGGACCGAGGAGGTGTACTCGCGCTACTGCCACGAGATGAGCGCGT 600

QY 1284 CTGCTGAGAGCTGATGGAGGTGCTCGGGGAGAGCTTGGCGATGTCGAGAGAGCGCGC 1343
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Db 601 CTGCTGAGAGCTGATGGAGGTGCTAGCGAGAGAGCTTGGCGAGAGCGCGTGGCG-----CGG 651

QY 1344 CACTACTTCGCGCATCTTCGAGCGACAGCTACATCATGCGCTCACTACACTACCG 1403
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Db 652 CGCCTACTTCGCGCATCTTCGAGCGAGAGCTACATCATGCGCTCACTACACTACCG 711

QY 1404 GGTGTCAGAGCGACCTCGACAGCTGGCGACCGGTGCGCGCTGCGACCGCGCTGCTC 1463
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QY 1464 ACCATCTCCAGCAGGACCGCTGCGCGCGCTGAGAGGTG-----GGGCGAGAGGGCGG 1517
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 772 ACCATCTCCAGCAGGACCGCTGCGCGCGCTGAGAGGTG-----GGGCGAGAGGGCGG 831

QY 1518 TGGCGCGCATCCGCGCTTCGCGCGCGCGCTGCTGCTCACTGCGCGACACTTTCATG 1577
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Db 832 TGGCGCGCATCCGCGCGCGCGCGCGCTTCTGCTGCTCACTGCGCGACACTTTCATG 891

QY 1578 GCGCTCTCCAGCGAGTACCGCAGCTGCTGCGCGCGCGCTGCTGCTCACTGCGCGAG 1637
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Db 892 GCGCTCTCCAAAGCGCGCTCAGGAGCTGCTCCACGCGCGCTCAACAGCGGGTG 951
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    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 952 GCAGCGCGCTGCTGGCGTCTTCTTCTTCTCCCGGAGATGAGAGCGTGTGGCGCGG 1011
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QY 1698 GAGGAGCTGCTGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1757
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1012 AAGGAGCTGCTGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1071
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1758 CTGGAGCTTACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1817
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1072 CTGGAGCTTACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1131
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1818 TGCGCTTA 1824
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1132 TGCGCTCA 1138

RESULT 2
LOCUS      BG322884          536 bp      mRNA      linear      EST 27-FEB-2001
DEFINITION EML_15_C10.b1_A002 Embryo 1 (EML) Sorghum bicolor cDNA, mRNA
sequence.
ACCESSION  BG322884
VERSION     BG322884.1  GI:13152562
KEYWORDS   EST.
SOURCE      sorghum.
ORGANISM   Sorghum bicolor
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
            clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE   1 (bases 1 to 536)
            Reid,S.P., Cordonnier-Pratt,M.-M., Gingle,A. and Pratt,L.H.
            An EST database from Sorghum: developing embryos
            Unpublished (2000)
            Contact: Cordonnier-Pratt MM
            Laboratory for Genomics and Bioinformatics
            The University of Georgia, Department of Plant Biology
            Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
            Tel: 706 542 1860
            Fax: 706 583 0210
            Email: mmpratt@uga.edu
            Sequences have been trimmed to exclude polyA, vector and regions
            below Phred quality 16. The threshold for highest quality sequence
            is 20.
            Seq primer: JEN REV
            High quality sequence stop: 508
            POLYA-No.
            Location/Qualifiers
                1..536
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                   /note="Organ: Embryos germinated for 24 hr; Vector:
                   pBluescript II from Lambda zap II; Site_1: XhoI; Site_2:
                   EcoRI; The library was made from poly-A RNA in the cloning
                   vector lambda zap II. Clones to be sequenced were
                   prepared by mass excision."
BASE COUNT      85 a  204 c  164 g  83 t
ORIGIN
Query Match      11.5%; Score 286.8; DB 12; Length 536;
Best Local Similarity 76.6%; Pred. NO. 1.8e-48;
Matches 418; Conservative 0; Mismatches 92; Indels 36; Gaps 4;

QY 1098 ACCAGCTTACAGGGCGCTTCGCGTCCAGCTGCGTGGAGAGGAGCGCTGCTGTCGG 1157
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 9 AGCAGCTTACAGGGCGCTTCGCGTCCAGCTGCCATGGAAGAGAGCGCTGCTGTCGGC 68
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QY 1158 TACTCATCGCTGGAGATGAGAGGCGGAGGCGGTGGGTGAGTACCTGTCGCGAAG 1217
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Db 69 TACT-----CGACAGCAGCGGCGGACGCGCTGCTGCTGCTACTCTCTCGACAG 122
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REFERENCE
AUTHORS      1 (bases 1 to 796)
              Wing, R., Close, T.J., Kleinohs, A., Wise, R., Begum, D., Frisch, D., Yu
              Y., Henry, D., Palmer, M., Rambo, T., Simmons, J., Oates, R., Choi, D.W.,
              Fenton, R.D., and Main, D.
TITLE        Development of a genetically and physically anchored EST resource
              for barley genomics: Morex cold-stressed seedling shoot cDNA
              library
JOURNAL      Unpublished (2001)
COMMENT      Contact: Wing RA
              Clemson University Genomics Institute
              Clemson University
              100 Jordan Hall, Clemson, SC 29634, USA
              Tel: 864 656 7288
              Fax: 864 656 4293
              Email: rwing@clemson.edu
              Total hq bases = 587
              Seq primer: AATTAAACCCCTCAATAAGGG
              High quality sequence stop: 644.
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                  /lab_host="TUC121"
                  /note="Vector: lambdaZAP; Site_1: EcoRI; Site_2: XhoI;
                  Seeds were surface sterilized then germinated under axenic
                  conditions in the dark at room temperature on filter paper
                  with water, nystatin and cerotaxime in covered
                  crystallization dishes. Five-day old seedlings were
                  incubated at 50C for 2 days. Shoots were then harvested,
                  total RNA was prepared, poly(A) RNA was purified, one
                  primary unamplified cDNA library was made, and 60000 pfu
                  were in vivo excised to give plasmids. These steps were performed in the TJ Close
                  phagemids. These steps were performed in the TJ Close
                  laboratory at the University of California, Riverside
                  (Choi, Close, Fenton). Phagemids were plated and picked at
                  the Clemson University Genomics Institute (CUGI) (Begum,
                  Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations
                  CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main
                  ). The sequence has been trimmed to remove vector sequence
                  and contains a minimum of 100 bases of phred value 20 or
                  above. For more details on library preparation and
                  sequence analysis see
                  http://www.genome.clemson.edu/projects/barley. To order
                  this clone see http://www.genome.clemson.edu/Also
                  see Close TJ, Wing R, Kleinohs A, Wise R (2001)
                  Genetically and physically anchored EST resources for
                  barley genomics. Barley Genetics Newsletter 31:29-30.
                  (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)
BASE COUNT   107 a 272 c 247 g 146 t 24 others
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Query Match          10.5%; Score 261.4; DB 12; Length 796;
Best Local Similarity 68.6%; Pred. No. 2.6e-43;
Matches 413; Conservative 0; Mismatches 159; Indels 30; Gaps 4;

QY 751 TGGTGTGTCAGCAGGAGGAGGTGTGTGTGACGCGCGGTGTGTGAGCGGCGAGACG 810
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Db 129 TGGTGGAGGCGATCATGTGTGACCGGTGTGTGACGCGCGGTGTGTGAGCGGCGAG 188
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QY 811 AGATCCCGTCGATTCATATGCGCGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 870
      ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 189 ACAATCCCGTCGATTCATATGCGCGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 248
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QY 871 ACCTGGAGGTGGCGTGTATGACGTGGG-----GCGGGGCGGAGAGGTGC 917
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Db 249 AGATGACGTCGCGCTCATCGACATCGCGGCGATGTCTCCGCGGAGACCCCGCGGCG 308
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QY 918 TC--GGTGTCCCGCAGGTGGGGAGGCGTCGCGAGAGCGACGCTTCTTCTTCTGGTGT 975
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Db 309 CCGAGGTGACGCGCTCGTGGCGAGGCGTCGCGAGCGCACGCTTCTTCCAGGTGCTCA 368
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QY 976 ACACGGCATCGAGCGCGCTCTGTGGAGGAGGCGCACCGTGCATGGAGCGCTTCTTCA 1035
      ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 369 ACCACGGCATCGAGCGCGCTCTGTGGCGGAGCGCACCGTGCATGGAGCGCTTCTTCA 428
      ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 1036 CGCTGCGCTGGGGGAGAGCAGCGGCGCGACGCGCGGGGAGAGAGCTCGGCTACG 1095
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Db 429 CCATGCGCTCCCGGAGAGACGCGCTCTGCGCGCGCCCGCGGAGTGTGCGGCTACG 488
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QY 1096 CCACGAGCTTCACGGGCGCTCTGCGGTCCAGCTGCGGTGGAAGAGAGCGCTCTTCC 1155
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Db 489 CCACGAGCTTCACGGGCGCTCTGCGGTCCAGCTGCGGTGGAAGAGAGCGCTCTTCC 548
      ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 1156 GGTACTCATCGCTGGAGTAGAGGCGGAGGCGGTGGTGGTACTCTGCTGGTGGCG 1215
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Db 549 GGTCTGTGCGCTC-----CGACCGCGCTCGTCTGCTGCTATCATCTGCGCA 596
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QY 1216 AGCTGGGCGCGAGCAGCGCGCTGGCGAGGTGTACTCTGCTACTCTCCACAGAGA 1275
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Db 597 CCGTCGGCGAGGACAC--CGCGCGCTGGGGAGGTGTAGCTCTACTCTCTCGGAGA 653
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QY 1276 TGAGCGCGCTGCTGCTGAGCTCATGAGGTCTCTCGGGAGAGCGCTGGGCGATCTCG 1335
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Db 654 TGAGCGCGCTGCTGCTGAGCTCATGAGGTCTCTCGGGAGAGCGCTGGGCGATCTCG 713
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QY 1336 AC 1337
Db 714 TC 715

RESULT 6
LOCUS       BE194605
DEFINITION BE194605.3 GI:16320901
            HVSMEh0086D02f Hordeum vulgare 5-45 DAP spike EST library
            HVCNA0009 (5 to 45 DAP) Hordeum vulgare cDNA clone HVSMEh0086D02f,
            mRNA sequence.
ACCESSION   BE194605
VERSION     BE194605.3
KEYWORDS    EST.
SOURCE      Hordeum vulgare
            Hordeum vulgare
ORGANISM    Hordeum vulgare
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
            ; Triticeae; Hordeum.
REFERENCE   1 (bases 1 to 577)
AUTHORS     Wing, R., Close, T.J., Kleinohs, A., Wise, R., Begum, D., Frisch, D., Yu
            Y., Henry, D., Palmer, M., Rambo, T., Simmons, J., Choi, D.W., Fenton
            R.D., Close, S.J., Oates, R. and Main, D.
TITLE       Development of a genetically and physically anchored EST resource
            for barley genomics: Morex 5-45 DAP spike cDNA library
JOURNAL     Unpublished (2001)
COMMENT     On Jun 26, 2000 this sequence version replaced gi:13187496.
            Contact: Wing RA
            Clemson University Genomics Institute
            100 Jordan Hall, Clemson, SC 29634, USA
            Tel: 864 656 7288
            Fax: 864 656 4293
            Email: rwing@clemson.edu
            Total hq bases = 162
            Seq primer: AATTAAACCCCTCAATAAGGG
            High quality sequence start: 21
            High quality sequence stop: 543.
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FEATURES
source

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FEATURES
source

Location/Qualifiers
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HVCNDA0009 (5 to 45 DAP)"
/tissue_type="5-45 DAP Spike"
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/note="Vector: lambdaZAP; Site 1: EcoRI; Site 2: XhoI;
Plants were grown in the greenhouse at the University of
California, Riverside (Fenton, SJ Close, TJ Close). Whole
spikes with awns trimmed were collected at 5, 10, 15, 20,
30 and 45 DAP (Fenton). Total RNA was prepared from each
pool, equal quantities of all six RNA pools were combined,
poly(A) RNA was purified from the mixture, one primary
unamplified cDNA library was made, and 1 million pfu were
in vivo excised to give pBluescript SK(-) cDNA phagemids
(Choi) in the TJ Close lab at the University of California,
Riverside. Phagemids were plated and picked at the Clemson
University Genomics Institute (CUGI) (Begum, Palmer,
Frisch, Atkins and Wing). Plasmid DNA preparations, DNA
sequencing and sequence analysis were performed at CUGI
(Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main).
The sequence has been trimmed to remove vector sequence
and contains a minimum of 100 bases of phred value 20 or
above. For more details on library preparation and
sequence analysis see
http://www.genome.clemson.edu/projects/barley. To order
this clone see http://www.genome.clemson.edu/orders Also
see close TJ, Wing R, Kleinbofs A, Wise R (2001)
Genetically and physically anchored EST resources for
barley genomics. Barley Genetics Newsletter 31:29-30.
(http://wheat.pw.usda.gov/gpages/bgn/31/cover.html)"

BASE COUNT 92 a 202 c 190 g 87 t
ORIGIN
Query Match 8.1%; Score 203.8; DB 10; Length 571;
Best Local Similarity 69.3%; Pred. No. 1.7e-31;
Matches 293; Conservative 0; Mismatches 127; Indels 3; Gaps 1;
QY 775 TGGTGTTCGACGCGCGGTGCTGACGCGGAGACGAGATCCCGTCGAGTTCATATGCG 834
Db 114 TCGTGTTCGACGCGCGGTGCTGACGCGGAGGACATCCCGCGCAGTTCATGTCG 173
QY 835 CGGCGGAGAGACCCCGGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 892
Db 174 CAGCGGAGAGACCCCGGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 233
QY 893 -CGTGGGCGGCGGCGGAGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 951
Db 234 TCGCGGCGGTCCTGCGCGCGGAGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 293
QY 952 GCGAGCGGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1011
Db 294 GCGAGCGGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 353
QY 1012 ACCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 1071
Db 354 ACCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 413
QY 1072 GCGCGGCGGAGAGTCGCGCTACGCGACGCTTCACGCGGCGCTTCGCTGCTGCTGCTGCTGCTG 1131
Db 414 GCTCGCGGAGAACCGCTACGCGCGGAGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 473
QY 1132 CGTGGAGGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1191
Db 474 COTGGAGGAGAGCATGCTCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 533
QY 1192 GCG 1194
Db 534 TCG 536

RESULT 11

BQ606563
LOCUS
DEFINITION BRY.2428 wheat EST endosperm library Triticum aestivum CDNA 5',
mRNA sequence.
ACCESSION BQ606563
VERSION BQ606563.1 GI:21555890
KEYWORDS EST,
SOURCE bread wheat.
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Triticum.
REFERENCE 1 (bases 1 to 567)
AUTHORS Clarke,B., Lambrecht,M. and Rhee,S.
TITLE Assessing the utility of Arabidopsis genomic information for
interpreting wheat EST sequences
JOURNAL Unpublished (2002)
COMMENT Contact: Lambrecht M
The Arabidopsis Information Resource
Carnegie Institution of Washington, Dept. of Plant Biology
260 Panama Street, Stanford, CA 94305, USA
Tel: 1 650 325 1521 x 251
Fax: 1 650 325 3748
Email: rheetacoma.stanford.edu.
FEATURES
Location/Qualifiers
1. .567
/organism="Triticum aestivum"
/cultivar="Wyuna"
/db_xref="taxon:4565"
/clone_lib="wheat EST endosperm library"
/tissue_type="endosperm"
/dev_stage="developing endosperm tissue 8, 10 and 12 DPA
(days post anthesis)"
/note="Vector: Bluescript II SK(-)"

BASE COUNT 80 a 200 c 203 g 83 t 1 others
ORIGIN
Query Match 8.0%; Score 200; DB 14; Length 567;
Best Local Similarity 66.7%; Pred. No. 1e-30;
Matches 354; Conservative 0; Mismatches 156; Indels 21; Gaps 4;
QY 775 TGGTGTTCGACGCGCGGTGCTGACGCGGAGACGAGATCCCGTCGAGTTCATATGCG 834
Db 46 TCGTGTTCGACGCGCGGTGCTGACGCGGAGAGACATCCCGCGCAGTTCGTCGTCG 105
QY 835 CGGCGGAGAGAGACCCCGGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 894
Db 106 CAGCGGAGAGACCCCGGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 165
QY 895 TGG-----GGCGGGGCGGAGAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 942
Db 166 TCGCGGCGGTCCTGCGCGGCGAGCGCTGCCACTGGCGGCTCCGTGACCTGGCGCGCG 225
QY 943 CGTGGAGAGGACCGCTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1002
Db 226 CGTGGAGAGGACCGCTTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 285
QY 1003 AGAGAGGACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1062
Db 286 CCAAGGCTACCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 345
QY 1063 CGAGCGGCGCGCGGAGAGGTGCGGCTAGCCAGAGCTTCACGCGGCGCTTCGCTGCTGCTGCTG 1122
Db 346 CGAGCGGCGCTTCGCGGAGAACACCGGCTACCGCGGAGCTTCGCTGGGCGGCTTCGCGA 405
QY 1123 CCAAGCTCCGCTGGAAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1182
Db 406 GCAAGCTCCGCTGGAAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 465
QY 1183 CGAGAGGAGCGCTGGGTGAGTACCTGCTGGGAGAGCTCGGGGCGGAGACGCGGCGCGCGC 1242

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Db 466 GCAG-----GTGTCGACTTCTGTCGCGTCTCGGCGAGGAGTAC---CGTGACA 516
QY 1243 TGGCGAGGTCTACTCGCGTACTGCGAGATGAGCGCGCTGCTGCTGG 1293
Db 517 TGGGAGGTGTGGCANGAGTACTGCGAGAGATGACGCGCTGGCGCTGG 567

RESULT 12
BG350197 655 bp mRNA linear EST 01-MAR-2001
LOCUS 084C04 Mature tuber lambda ZAP Solanum tuberosum cDNA, mRNA
DEFINITION
ACCESSION BG350197
VERSION BG350197.1 GI:13178939
KEYWORDS EST.
SOURCE potato.
ORGANISM Solanum tuberosum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
1. (bases 1 to 655)
AUTHORS Nielsen,K.L., Crookshanks,M., Emmersen,J. and Welinder,K.G.
TITLE EST-sequencing of mature potato tuber (Var. Kuras)
JOURNAL Unpublished (2000)
COMMENT Contact: Karen G. Welinder
Institit for bioteknologi
Aalborg Universitet
Sohngaardsholmsvej 49, 9000 Aalborg, Denmark
Tel: +45 96358467
Fax: +45 98141808
Email: kgw@bio.auc.dk
Sequenced from the 5' end.
High quality sequence stop: 655
POLYA-No.

FEATURES
    source
    1. .655
        /organism="Solanum tuberosum"
        /cultivar="Field grown Kuras"
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        /clone_lib="Mature tuber lambda ZAP"
        /tissue_type="tuber"
        /notes="Vector: Lambda ZAP"
BASE COUNT 224 a 129 g 120 g 180 t
ORIGIN
    Query Match 7.9%; Score 196.8; DB 12; Length 655;
    Best Local Similarity 63.3%; Pred. No. 4.5e-30;
    Matches 300; Conservative 0; Mismatches 174; Indels 0; Gaps 0;

QY 1360 TCTTCAGCGCAAGCACTCCATCATCGGCTCACTACTACCGCGTGCAGAGCGCAC 1419
Db 9 TATTGGAAGAAATGATTGCAATGAGACTCACTACTATCCACCATGFCAGAAACGG 68
QY 1420 TCACACGCTGGGACCGGTCGCGACTGCGACCCACCTCCCTCACATCTCCACGAG 1479
Db 69 AGCTCACTTAGGACGCGGCGCTCATGTGTGACCCCAACATCAATTAACAATTCCTCATCAAG 128
QY 1480 ACCACCTCGCGCGCTGAGGTGTGGCGAGGCGGCTGCGCGCATCGCGCTCGCC 1539
Db 129 ATTGTGTGCGGAGCTTCAAGTTTTTGTGATGATGATGATGATGATGATGATGATGAT 188
QY 1540 CCGGGGCGCTCGTCTCAACGTGGGAGACACCTTTCATGCGCTCTCCAAAGCGCAGTACC 1599
Db 189 TCAATGCATTTTGTGTTAAATGAGGAGACACATNTATGGCGCTATCAATGGAAGATACA 248
QY 1600 GCACTGCTCGTCCACCGGCGGTGTGTCAACAGCAGCGCGCTGCGCGCTGCTGCGCTTCT 1659
Db 249 AAAGTTGCTGCACAGAGAGTAGTAACAACAAGACTCTCTAGAAAATACACTTGTCTTCT 308
QY 1660 TCTCTGTCGCGGAGATGACAGCTGTGCGCGCGCGCGGAGAGCTGGTGCAGCACCACC 1719
Db 309 TTCTTTGTCCAAACAAGATAGGTGTGAGGCCCAACCAATGAATTGTTGAGCTCCACA 368

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QY 1720 ACCGAGGTGTACCGGACTTCACGTGCGGCGGCTGCTGGACTTCACGACGCGCCT 1779
Db 369 ACCCTCGAATATATCTGATTTCACATGCGCTACTCTCTTGATTTACTCAAAACATT 428
QY 1780 ACAGGCGGACATCGCAGCTTCACGCTTCAGGCTTCTCCGACTGCTTAATCATCATC 1833
Db 429 ATAGAGCTGATATGACACTCTTCAAAACATTTCAAATNGGCTCATGATCAAC 482

RESULT 13
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LOCUS WHE0056_E02_I04Zs Wheat endosperm cDNA library Triticum aestivum
DEFINITION
ACCESSION BE422495
VERSION BE422495
KEYWORDS EST.
SOURCE bread wheat.
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
; Triticeae; Triticum.
1. (bases 1 to 517)
AUTHORS Altenbach,S., Anderson,O.D., Chao,S., Galili,G., Han,P.S., Hsia
,C.C., Kang,Y., Lazo,G.R., Miller,R., Rausch,C.J., Seaton,C.L. and
Tong,J.C.
TITLE The structure and function of the expressed portion of the wheat
genomes - Endosperm cDNA library
JOURNAL Unpublished (2000)
COMMENT Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
Email: oanderson@pw.usda.gov
Sequence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: Stratagene SK primer.

FEATURES
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    1. .517
        /organism="Triticum aestivum"
        /cultivar="Cheyenne"
        /db_xref="taxon:4565"
        /clone="WHE0056_E02_I04"
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        /tissue_type="Endosperm"
        /dev_stage="5 to 30 days post anthesis seed"
        /lab_host="E. coli SOLR"
        /notes="Vector: Lambda ZAP II, excised phagemid; Site_1:
        EcoRI; Seeds collected, endosperm isolated, and RNA
        prepared by Susan Altenbach. Library constructed by
        Stratagene, Inc. Plasmid DNA preparations and DNA
        sequencing were performed in the OD Anderson lab."
BASE COUNT 96 a 149 c 161 g 111 t
ORIGIN
    Query Match 7.6%; Score 191.2; DB 10; Length 517;
    Best Local Similarity 71.5%; Pred. No. 6.6e-29;
    Matches 266; Conservative 0; Mismatches 103; Indels 3; Gaps 1;

QY 1460 GCTCACATCTCCACGAGCACCACGCTCGCGCGCTGAGGTGTGGCGAGGCGGTG 1519
Db 517 GCTGACGCTGCTCCACGAGCAGCGCTCGCGGGCTGAGGTGTTCACGCGCGCGCTG 458
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Db 457 GCSCGCGGTGCGCGCGCGGAGCGACGCCCTTCGCTCAACATCGGCGACACCTTCTCGCG 398
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Db 397 GCTCAACCAAGCGCGCGCCACATCATGCTCCACCGCGCGGTGCTCAACAGCAGCGCTGCG 338

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QY 1640 TCGCGCTCGTGGCTTCTTCTCTGCCCCGAGATGACACGGTGTGTGCGCCCGCGGA 1699
Db 337 CGCGAGTGGCTTCACTTCTTCTCAACCCGAGCTGGACCGCTGTGTGCGCCCGCGG 278
QY 1700 GGAGCTG---GTGACGACACACACCCCGAGGCTGTACCCGAGCTTACGTTGGCGGCGCT 1756
Db 277 CGAGCTGTCTGCGCTGCGACGCGCGCGCGCGCTGTACCCGAGCTTCACTTGGCTGAAT 218
QY 1757 GTGAGCTTACGAGCGCGCTTACAGGCGCGACATGCGCACGCTTACAGCGCTTCCCGA 1816
Db 217 CTCTGAGTTACAGAGAGCACTACCGCTCTGACTGGAGAGCCCTGGATGCAATGCGCTC 158
QY 1817 CTGGCTTAATCA 1828
Db 157 GTGATCAATCA 146

RESULT 14
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LOCUS BE414214 686 bp mRNA linear EST 24-JUL-2000
DEFINITION SCU007.E01.R990714 ITFC SCU Wheat Endosperm Library triticum
aestivum cDNA clone SCU007.E01, mRNA sequence.
ACCESSION BE414214
VERSION BE414214.1 GI:9412060
KEYWORDS EST.
SOURCE bread wheat.
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Triticum.
REFERENCE 1 (bases 1 to 686)
AUTHORS Anderson,O.A., Appels,R., Bailey,P., Blake,T., Close,T., Cloutier
,S., Dubcovsky,J., Feuillet,C., Gale,M., Graner,A., Gustafson,P.,
Herrmann,R.G., Holton,T., Jacquemin,J.M., Jia,J., Joudrier,P.,
Langridge,P., Lazo,G.R., Lin,J.J., McGuire,P., Ogihara,Y.,
Pechioni,N., Qualset,C., Schuch,W., Selvaraj,G., Shariflou,M.,
Sorrells,M., Warburton,M. and Wenzel,G.
TITLE International Triticale EST Cooperative (ITEC): Production of
Expressed Sequence Tags for Species of the Triticeae
JOURNAL Unpublished (2000)
COMMENT Contact: Holton T
Centre for Plant Conservation Genetics, Southern Cross University
PO Box 157, Lismore NSW 2480 AUSTRALIA
Tel: 61 2 6620 3409
Fax: 61 2 6622 2080
Email: tholton@scu.edu.au
International Triticale EST Cooperative (ITEC)
http://wheat.pw.usda.gov/genome.
FEATURES
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1. 686
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/notes="Vector: Bluescript II SK(-)"
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Best Local Similarity 68.1%; Pred. No. 4.6e-28;
Matches 294; Conservative 0; Mismatches 126; Indels 12; Gaps 2;

QY 775 TGTGTTCAGCGCGGCTGTGAGCGGGCAGACGAGATCCCTCCAGTTCATATGCGC 834
Db 159 TCGTGTTCAGCGCGGCTGTGAGCGGGCTGTGAGGAGATCGCGTCCCGGCTGTGCGC 218
QY 835 CGCGGAGAGAGAGCCCGCTGCGGTGTGAGGAGCTGGAGTGGCGCTGATCAGCAGC 894
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QY 895 TGG-----GGCGGGCGGAGAGTCTGTCGTGG--TCCGCGAGTGGGGAGG 942
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QY 943 CFTGGCAGAGCAGCGGTCTTCTCTGTGTGTTTAAACACGCGATCGAGGGCGGCTGCTGG 1002
Db 339 CFTGGCAGAGCAGCGGTCTTTCAGGCTGTGACACGAGGGGTGGACCGGGGCTGCTGG 398
QY 1003 AGAGGGCGACCGGTGTCATGGAGCCCTTTCACGCTCCGCTGGGGGAGAGACAGCGGG 1062
Db 399 CCAAGCGCTACCGGTGTGCGAGCCCTTTCAGCGCTGCCGCTGCCGCGAGAGCAGCGG 458
QY 1063 CGCAGGGCGCGGGGAGAGCTGCGGCTAGCCAGCAGCTTACGCGGCGCTTGGCGT 1122
Db 459 CGCAGGGCGCGGCTGCGGAGACACGCGGTAGCGGCGAGCTTCTGTTGGGCGGGTCGGCA 518
QY 1123 CCAAGCTCCGTGGAAGGAGACGCTGTCTCTCCGTACTCATCTCGGTGGAGATGAGAGG 1182
Db 519 GCAAGTCCCTGGAGGAGACCGCTGTCTTCACTGTCTCCGCGCGCGGANGGCGCC 578
QY 1183 GCGAGGAGGGCG 1194
Db 579 GCAAGGTCTGCG 590

RESULT 15
BQ402912
LOCUS BQ402912 700 bp mRNA linear EST 22-MAY-2002
DEFINITION GA_Ed0052C12f Gossypium arboreum 7-10 dpa fiber library Gossypium
arboreum cDNA clone GA_Ed0052C12f, mRNA sequence.
ACCESSION BQ402912
VERSION BQ402912.1 GI:21090599
KEYWORDS EST.
SOURCE Gossypium arboreum.
ORGANISM Gossypium arboreum.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
REFERENCE 1 (bases 1 to 700)
AUTHORS Wing,R.A., Frisch,D., Yu,Y., Main,D., Rambo,T., Simmons,J., Henry
,D., Wood,T.C., Leslie,A. and Wilkins,T.A.
TITLE An integrated analysis of the genetics, development, and evolution
of the cotton fiber
JOURNAL Unpublished (2000)
COMMENT Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total High Quality bases = 572
Seq primer: TAATACACTCACTATAGG
High quality sequence start: 7
High quality sequence stop: 680.
Location/Qualifiers
1. 700
/organism="Gossypium arboreum"
/strain="AKA"
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/clone="GA_Ed0052C12f"
/tissue_type="Fibers isolated from bolls harvested 7-10
dpa"
/lab_host="E. coli"
/notes="Vector: pBR-CMV; Site_1: EcoRI; Site_2: XhoI"
BASE COUNT 194 a 148 c 171 g 186 t 1 others
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Best Local Similarity 59.9%; Pred. No. 8.8e-28;
Matches 371; Conservative 0; Mismatches 230; Indels 18; Gaps 3;

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QY 928 GCCAGTGGGAGGCGGTGGAGAGGAGCGCTTCTTCTCGTGGTGTAAACACAGGCAFCG 987
Db 100 GGCTGGTGGGAGGCAATGTGCGCAGCATGTTCTTCTTGTGTGTTAATCATGAGTGG 159
QY 988 AGGCGGCGCTCTGCGAGGAGGCGCAGCGGTGATGAGAGCGCTTCTTACGCTGGCGCTGG 1047
Db 160 ATGCACACTGGTGGCTGATGCTCAGAGTTATATGGGTAACTTCTTGAATGGCAATCA 219
QY 1048 GGGAGAGCAGCGGCGGCGCAGCGCGGCGGAGAGCTGGCTACGCCAGCAGCTTCA 1107
Db 220 ATGATAAGCAAAAGGCTCAGAGGAACTTGTGAGCACTGTGGATATGCTAGTAGCTTCA 279
QY 1108 CGGGGCGCTTCGCTCCAAAGCTCCCTGGAAGAGAGAGCTGTGCTCCGGTACTCATCG 1167
Db 280 CTGCTAGATTACCTTCCAAAGCTCCATGGAAGGAAAGCTTCTTTCGGTATTC--- 335
QY 1168 CTGGAGATGAGAGGCGGAGGCGGTGGTGTAGTACTGTGCGGAAAGCTCGGGGCGG 1227
Db 336 --GCTGACAAAACCTCATCCAGATTGTTGAAGACTACCTGTGTGCAATTTGGGAGATG 393
QY 1228 AGCAGCGGCGGCGGTGGGAGGTGTACTCCGCTACTGCCAGAGATGAGCCGCTGT 1287
Db 394 AATTC---AAGCAATTCGGAGGCTTTACCAAGATTACTCGAGGCAATGAGCAAGCTAT 450
QY 1288 CGCTGAGCTGTGAGGTGCTCGGGAGAGCGCTGGGCATGCTGGAGACCGGCGCCACT 1347
Db 451 CTCTAGGGATATGAGGCTATTAGCCATTAGTCTTGGCGTAGGAGATCNC----- 501
QY 1348 ACTTCGGCGATTTCTCCAGCGCAAGCACTCCCATCATCGCCTCAACTACTACCGCGGT 1407
Db 502 ATTTCAAGGAAATTTTTCAGGAAATGAATCAATTAATGAGCTCAATTAATACCCACCAT 561
QY 1408 GCCAGAGCCACTCGACACCTGGGACCGGTCCGCACTGCGACCCCACTCGCTCACA 1467
Db 562 GCCAAAACCAAGACTCACTTANGAACAGGGCCTCATTTGGGATCCAAOCTCATTAACA 621
QY 1468 TCCTCCACAGACCACTCGCGGCGCTGGAGGTGTGGGCGGAGGGGCGGTGGCGCGCA 1527
Db 622 TCCTTCACCAAGACCGATTTGGTGTCTTCAAGTGTGTTAGACAAATGATGCGGTTCAA 681
QY 1528 TCGGCGCTCGCCCGGGGC 1546
Db 682 TTAGCCCAATCTCGAAGC 700

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Search completed: March 26, 2003, 07:52:50
Job time : 2570.09 secs

GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 26, 2003, 04:38:30 ; Search time 61.8613 Seconds
(without alignments)
12398.686 Million cell updates/sec

Title: US-09-702-134-7212_COPY_28000_30500

Perfect score: 2501
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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/PCFUS_COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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4	271	10.8	1490	2	US-08-553-367A-5
5	271	10.8	1490	4	US-09-295-306-5
6	271	10.8	1490	4	US-09-734-719-5
7	226.4	9.1	1395	2	US-08-553-367A-1
8	226.4	9.1	1395	4	US-09-295-306-1
9	226.4	9.1	1395	4	US-09-734-719-1
10	94.4	3.8	1926	4	US-09-249-585A-2
11	94.4	3.8	2580	3	US-09-050-863-2
12	94.4	3.8	2580	4	US-09-359-081-2
13	94.4	3.8	5452	2	US-09-130-114-1
14	94.4	3.8	9600	4	US-08-910-647-1
15	94.4	3.8	9600	4	US-09-620-925-1
16	94.4	3.8	10596	1	US-07-884-811-15
17	94.4	3.8	10596	1	US-07-885-971-15
18	94.4	3.8	10596	1	US-08-087-783A-15
19	94.4	3.8	10596	1	US-08-194-088B-15
20	94.4	3.8	10596	2	US-08-194-087-15
21	94.4	3.8	10596	5	PCT-US93-04648-15
22	94.2	3.8	1181	2	US-08-632-598-2
23	94.2	3.8	1181	4	US-09-231-240-2
24	90	3.6	1926	4	US-09-249-585A-4
25	90	3.6	1931	2	US-09-130-114-2
26	79.8	3.2	1505	1	US-07-915-246-1
27	78.2	3.1	2793	1	US-08-209-747-1

28	78.2	3.1	2793	1	US-08-458-298-1	Sequence 1, Appli
29	77.2	3.1	672	4	US-09-454-034-9	Sequence 9, Appli
30	73.8	3.0	174	2	US-08-553-367A-12	Sequence 12, Appli
31	73.8	3.0	174	4	US-09-295-306-12	Sequence 12, Appli
32	73.8	3.0	174	4	US-09-734-719-12	Sequence 12, Appli
33	72.6	2.9	888	4	US-08-785-907A-2	Sequence 2, Appli
34	72.6	2.9	2888	4	US-08-785-907A-1	Sequence 1, Appli
35	64.6	2.6	2338	1	US-08-425-069-1	Sequence 1, Appli
36	64.6	2.6	2338	2	US-08-317-844B-1	Sequence 1, Appli
37	64.2	2.6	7218	1	US-08-232-463-14	Sequence 14, Appli
38	64	2.6	1228	2	US-08-823-986A-1	Sequence 1, Appli
39	64	2.6	1228	3	US-08-784-385-1	Sequence 1, Appli
40	64	2.6	1270	5	PCT-US95-10403-1	Sequence 1, Appli
41	64	2.6	1663	2	US-08-823-986A-3	Sequence 3, Appli
42	64	2.6	1663	3	US-08-784-385-3	Sequence 3, Appli
43	64	2.6	1703	5	PCT-US95-10403-3	Sequence 3, Appli
44	62.6	2.5	470	4	US-09-615-192A-149	Sequence 149, App
45	62.6	2.5	2830	2	US-09-010-928B-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-08-553-367A-3
; Sequence 3, Application US/08553367A
; Patent No. 5939539
; GENERAL INFORMATION:
; APPLICANT: Theodor LANGE et al.
; TITLE OF INVENTION: GA 20-OXIDASE GENE SEQUENCES (As Amended)
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
; STREET: 2033 K Street, N.W., Suite 800
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,367A
FILING DATE: No. 5939539 September 27, 1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lee Cheng

REGISTRATION NUMBER: 40,949
REFERENCE/DOCKET NUMBER: 49/FDA.5M2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-721-8200
TELEFAX: 202-721-8250
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1259 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Arabidopsis thaliana
IMMEDIATE SOURCE:
CLONE: pAT2301
US-08-553-367A-3


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QY 1779 TACAGGCGGACATGCGCAGCTTCAGGCTTCCGAGTGGCTTA 1824
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Db 1086 TATAGCAGACATGACACTTCCAGGCTTTTCAGATGGCTCA 1131
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RESULT 3

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US-09-734-719-3
; Sequence 3, Application US/09734719
; Patent No. 6455675
; GENERAL INFORMATION:
; APPLICANT: Theodor LANGE et al.
; TITLE OF INVENTION: GA 20-OXIDASE GENE SEQUENCES (As Amended)
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
; STREET: 2033 K Street, N.W., Suite 800
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09734,719
; FILING DATE: 13-Dec-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/295,306
; FILING DATE: April 21, 1999
; APPLICATION NUMBER: 08/553,367
; FILING DATE: No. 6455675ember 27, 1995
; APPLICATION NUMBER: PCT/EP94/01664
; FILING DATE: May 24, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee Cheng
; REGISTRATION NUMBER: 40,949
; REFERENCE/DOCKET NUMBER: 2000-1678/LC/01784
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-721-8200
; TELEFAX: 202-721-8250
; TELEX: <Unknown>

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; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1259 base pairs
; TYPE: nucleic acid
; TOPOLOGY: single
; STRANDEDNESS: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Arabidopsis thaliana
; IMMEDIATE SOURCE:
; CLONE: PAT2301
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-734-719-3

Query Match 11.78; Score 292.4; DB 4; Length 1259;
Best Local Similarity 60.08; Pred. No. 2.2e-54;
Matches 532; Conservative 0; Mismatches 336; Indels 18; Gaps 2;

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Db 264 GAGCGCTGTAAGAACACGCGTTTCTTCTGTTGTTCAATCAAGCGCATCGAGGAGCTT 323
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QY 999 CTGGAGAGCGCCACCGGTCATGAGACGCTTCTTCAAGCTGCGCGCTGGGGGAGAGACAG 1058
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Db 324 ATATCAGACGCTCATGAATACACGAGCGGCTTCTTGATATGCTCTCTCCGAAACAG 383
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Db 444 TCCACCAAGCTTCCATGGAAGAGACCTTTCTTCCGGT-----TTGCGAGCAG 494
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QY 1239 CGGCTGGGCGGCTGCTACTCGCGCTACTGCCAGAGATGAGCGCGCTGCTCGTGGAGCTG 1298
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QY 1299 ATGAGAGTCTCGGGGAGAGCCTGGGCATCGTGGAGAGCCGGGCGCACTACTTCCGGCA 1358
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Db 615 ATGAGAGCTTCTCGGCTAAGTTTAGC-----GTAAACGGGACTACTTTAGAGAG 665
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QY 1359 TTCTTCCAGCAACGACTCCATCATCGGCTCAACTACTACCGGCGTCCGAGAGCCA 1418
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Db 666 TTTTTCGAGAAACGATTCAATATGAGACTGAATTAACCTCCATGTATATAAACCA 725
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QY 1419 CTCGACAGCTGGGACCGGTCGCACTGGACCGCCACCTCGCTCACCATCTCCACAG 1478
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Db 726 GATCTCACACTAGGAACAGGACCTCATTTGATCCCAACATCTCTTACCATCTTCACCA 785
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QY 1479 GACACAGCTCGGCGGCTGGAGGCTGGGGGAGGGGGGGGGGGGGGGGGGGGGGGGG 1538
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Db 786 GACCATGTTAATGGCTTCAAGCTTTGTGGAATCAATGCGCTCCATTCGTCCCAAC 845
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QY 1539 CCGGGGCGCTGCTGTCACAGCTCGGCGCACCTTCATGGCGCTTCCACGCGCAGGTAC 1598
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Db 846 CCCAAGGCTTTGTGTCATATCGGCGTACTTTTCATGGCTCTATCGAAGATAGATAC 905
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QY 1599 CGCAGTGTGCTGCACCGGGGGTGGTCAACAGCACGGCGCTCCGCTCGTGGCGCTTC 1658
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Db 906 AAGAGCTGCTGCACCGGGCGGTGGTGAACAGCAAGAGCGAGAGAGTCACTTGCATTTC 965
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QY 1659 TTCTCTGCGCGGAGATGAGACAGGCTGGTGGCGCGCGCGGAGAGAGCTGTGTCAGCAG 1718
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Db 966 TTCTCTGTCCGAAAGAAAGACAGAGTAGTAGTACGCCACCGGAGAGAGCTTTTGGACAG 1025
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QY 1719 CACCGAGGCTGACCGGAGCTTCACGTGGGCGCGCTGCTGGCTTCACGAGCGCCAC 1778
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Db 1026 ACATCAAGAGATACCTGATCTACATGCTATGTTCTGATTCCTACTCAGAAACAT 1085
 QY 1779 TACAGGCGGACGACGCGCTTACGCGCTTCTCCGACTGGCTTA 1824
 Db 1086 TATAGAGCAGACATGAACATCTCCAGCCCTTTCAGATTGGCTCA 1131

RESULT 4

US-08-553-367A-5
 ; Sequence 5, Application US/08553367A
 ; Patent No. 5939539
 ; GENERAL INFORMATION:
 ; APPLICANT: Theodor LANGE et al.
 ; TITLE OF INVENTION: GA 20-OXIDASE GENE SEQUENCES (As Amended)
 ; NUMBER OF SEQUENCES: 19
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
 ; STREET: 2033 K Street, N.W., Suite 800
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: U.S.A.
 ; ZIP: 20006
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: MS-DOS
 ; SOFTWARE: Wordperfect 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/553.367A
 ; FILING DATE: No. 5939539 member 27, 1995
 ; CLASSIFICATION: 800
 ; PRIOR APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Lee Cheng
 ; REGISTRATION NUMBER: 40,949
 ; REFERENCE/DOCKET NUMBER: 49/FD4.5M2
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-721-8200
 ; TELEFAX: 202-721-8250
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1490 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA to mRNA
 ; HYPOTHEetical: NO
 ; ANTI-SENSE: NO
 ; ORIGINAL SOURCE:
 ; ORGANISM: Arabidopsis thaliana
 ; IMMEDIATE SOURCE:
 ; CLONE: PAT2353
 ; US-08-553-367A-5

Query Match 10.8%; Score 271; DB 2; Length 1490;
 Best Local Similarity 56.5%; Pred. No. 1e-49;
 Matches 593; Conservative 0; Mismatches 435; Indels 21; Gaps 4;

QY 778 TGTTCAGCGCGGCTGCTGAGCGGACGAGATCCCGTCGCACTTCATATGCGCG 837
 Db 175 TCCTTAACCTCTCTCTTCTTAACCTCCAAATCCCAACCAATTCATTGGCCAG 234
 QY 838 CGAG 897
 Db 235 ACAG 291
 QY 898 GGGCGGGGCGGAG 957
 Db 292 CAAGCCAG 351

QY 958 GCTTCTCTCTGTTGTTAAACCAGCATCGAGGCGGCTCTCTGAGGAGGCGACCGGT 1017
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 QY 1018 GATGAG 1077
 Db 412 TGTGAG 471
 QY 1078 GGGAG 1137
 Db 472 GTGAG 531
 QY 1138 AG 1197
 Db 532 AG 585
 QY 1198 GTGAG 1257
 Db 586 AAGATTACTTTTCCGANTACATTAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 642
 QY 1258 CGCGTACTGCGACAGAGATGAGCGGCTCTCTGAGAGAGAGAGAGAGAGAGAG 1317
 Db 643 AAGACTATTGTGAG 702
 QY 1318 GCTGAG 1377
 Db 703 GTTAGGCGGTAACCGAG-----ACTATTCCGAGAGATTTTCGAGAGAGAGAGAT 753
 QY 1378 CATCATCGGCTCACTACTACTACCGGCGTGCAGAGAGAGAGAGAGAGAGAGAG 1437
 Db 754 CGATAATGAGGCTCAATCATTTATCTCCATGCAACACAGATCTCAAGTAGGTACAG 813
 QY 1438 GTCCGACTGCGACCGGCGGCTCTCCATCCTCCAGAGAGAGAGAGAGAGAGAGAG 1497
 Db 814 GACCTCATTTGATCCAAAGTCTTTGACCATCTTCAATCAAGAGAGAGAGAGAGAG 873
 QY 1498 AGTGTGAG 1557
 Db 874 AAGTCTTTGTGAG 933
 QY 1558 AGTGTGAG 1617
 Db 934 ATATTGAG 993
 QY 1618 CGTCTCTCAACAG 1677
 Db 994 CGGTTGTATAG 1053
 QY 1678 ACAGGAG 1737
 Db 1054 ACAAGTGTGAG 1113
 QY 1738 ACTTCAGTGTGAG 1797
 Db 1114 ACTTCAGTGTGAG 1173
 QY 1798 CGTTCAGGAG 1826
 Db 1174 CTCTCGATTCTCTTCTAATTTGGGTTATT 1202

RESULT 5

US-09-295-306-5
 ; Sequence 5, Application US/09295306
 ; Patent No. 6198021
 ; GENERAL INFORMATION:
 ; APPLICANT: Theodor LANGE et al.
 ; TITLE OF INVENTION: GA 20-OXIDASE GENE SEQUENCES (As Amended)
 ; NUMBER OF SEQUENCES: 19
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
 ; STREET: 2033 K Street, N.W., Suite 800

CITY: Washington
 STATE: D.C.
 COUNTRY: U.S.A.
 ZIP: 20006
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: Wordperfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/295,306
 FILING DATE: 08/553,367
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/553,367
 FILING DATE: No. 6198021ember 27, 1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Lee Cheng
 REGISTRATION NUMBER: 40,949
 REFERENCE/DOCKET NUMBER: 49/DIV-FD4.5M2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-721-8200
 TELEFAX: 202-721-8250
 TELEX:
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1490 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA to mRNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Arabidopsis thaliana
 IMMEDIATE SOURCE:
 CLONE: PAT2353
 US-09-295-306-5

Query Match 10.8%; Score 271; DB 4; Length 1490;

Best Local Similarity 56.5%; Pred. No. 1e-49;
Matches 593; Conservative 0; Mismatches 435; Indels 21; Gaps 4;

QY 778 TGTTCAGACGCGCGGTGTGTCAGGCGGAGAGATCCGTCGACGTTTCATATGCGCG 837
 DB 175 TCCTTAACCTCTCTTCTTAACCTCCATCCCAATCCCAACCAATTCATTGGCCAG 234
 QY 838 CGAG 897
 DB 235 ACAG 291
 QY 898 GGGCGGGGCGGAG 957
 DB 292 CAG 351
 QY 958 GCTTCT 1017
 DB 352 GCTTCT 411
 QY 1018 GCATGACGCGCT 1077
 DB 412 TGATGGAAGTTCT 471
 QY 1078 GGGAG 1137
 DB 472 GTGAG 531
 QY 1138 AG 1197
 DB 532 AGGAG 585
 QY 1198 GTGAG 1257

DB 586 AGATTACTTTTCCGATACATTAGGACAAAGAGTTCCG---AGCAGTTTGGAGAGTGATTC 642
 QY 1258 CGCGTACTGCGACGAGATGAGCGCGCTGTCTGCTGGAGCTGATGGAGGTGCTCGGGGAGA 1317
 DB 643 AGACTATTTGTGAAGCAATGAGTTCTCTACTCAAGATCATGAGGCTTCGGGCTTAA 702
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 DB 703 GTTAGGCGTAACCGAGS-----ACTATTTCCGAGGATTTTTCGAGAGAGAACGATT 753
 QY 1378 CATCATGCGCTCACTACTACCGGCGTGCAGAGGCGCATCGACACGCTGGGCAACCG 1437
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 QY 1438 GTCCGACTGCGACCCACCTCGCTCAATCTCTCCAGGAGGAGGAGGAGGAGGAGGAGG 1497
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 DB 874 AAGTCTTTGTCGACAAATCAATGGAATCAATTCGTCCTCAATGCGGCTTTTCGTTGCA 933
 QY 1558 AGTGGGCGACACCTTCATGCGCTCTCCAGCGCAGGTACCGCAGCTGCTGCGACCGGG 1617
 DB 934 ATATTGGTGACACTTTTCATGCTCTATCGAAGCGGATATTCAGAGCTGTTGCATAGAG 993
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 DB 994 CGTGTGTGATAGAGAGAGCGGAGAAATCGATGGCGTTTCTTGTCTGCGGAGAAAG 1053
 QY 1678 ACAGGCTGTGCGCGCGCGGAGGAGGAGTGTGTCGAGGAGGAGGAGGAGGAGGAGG 1737
 DB 1054 ACAAGTGTGAACCAACCAAGTATTTTGGAGAGATGAAACAAAGAAATACCCCTG 1113
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 DB 1114 ACTTCACGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1173
 QY 1798 CGTTCAGGCTTCTCGGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1826
 DB 1174 CTCGATGCTCTTCTTAATTTGGTTATT 1202

RESULT 6
 US-09-734-719-5
 ; Sequence 5, Application US/09734719
 ; Patent No. 6455675
 ; GENERAL INFORMATION:
 ; APPLICANT: Theodor LANGE et al.
 ; TITLE OF INVENTION: GA 20-OXIDASE GENE SEQUENCES (As Amended)
 ; NUMBER OF SEQUENCES: 19
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: U.S.A.
 ; ZIP: 20006
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: MS-DOS
 ; SOFTWARE: Wordperfect 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/734,719
 ; FILING DATE: 13-Dec-2000
 ; CLASSIFICATION: <unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 09/295,306
 ; FILING DATE: April 21, 1999
 ; APPLICATION NUMBER: 08/553,367
 ; FILING DATE: No. 6455675ember 27, 1995
 ; APPLICATION NUMBER: PCT/BF94/01664

RESULT 8
US-09-295-306-1

[illegible]

Search completed: March 26, 2003, 13:12:32
Job time : 97.8613 secs

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	226.4	9.1	1161	10	US-09-371-307-77		Sequence 77, Appl
2	153.2	6.1	1077	10	US-09-371-307-8		Sequence 8, Appl
3	129	5.2	811	10	US-09-371-307-71		Sequence 71, Appl
4	84.8	3.4	12733	9	US-10-032-393-47		Sequence 47, Appl
5	84.8	3.4	12739	9	US-10-032-393-8		Sequence 8, Appl
6	81.2	3.2	266	10	US-09-923-875-1829		Sequence 1829, Ap
7	80	3.2	768	9	US-09-938-842A-812		Sequence 812, App
8	74.8	2.9	1179	9	US-09-938-842A-1511		Sequence 1511, Ap
9	73.2	2.9	276	10	US-09-294-093B-5184		Sequence 5184, Ap
10	73.2	2.9	1050	9	US-09-938-842A-2672		Sequence 2672, Ap
11	73	2.9	446	10	US-09-864-761-20699		Sequence 20699, A
12	71.6	2.9	1075	10	US-09-864-761-19241		Sequence 19241, A
13	71.6	2.9	1403	10	US-09-864-761-19241		Sequence 2513, Ap
14	71.4	2.9	1030	10	US-09-371-307-5		Sequence 5, Appli
15	71.4	2.9	1852	10	US-09-369-853-4		Sequence 4, Appli
c 16	68.2	2.7	1635	10	US-09-864-761-20241		Sequence 20241, A
c 17	68.2	2.7	1973	10	US-09-864-761-3471		Sequence 3471, Ap
c 18	68.2	2.7	2283	9	US-09-938-842A-1691		Sequence 1691, Ap
c 19	68.2	2.7	2283	10	US-09-887-576-645		Sequence 645, App

RESULT 7
US-09-938-842A-812
Sequence 812, Application US/09938842A
Patent No US20020160378A1
GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: K'eps, Joel
APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED
TITLE OF INVENTION: SAME, AND METHOD
FILE REFERENCE: SCRI1300-3
CURRENT APPLICATION NUMBER: US/09/938
CURRENT FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: US 60/227,8
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,5
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,1
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379

QY 1450 ACCCCACCTCGTCACTCACTCCACAGGACACAGTGGCGGCTGGAGTGTGGCGG 1509
 Db 96 ACATGAGCAGCTCAGCTCCCTCTGTCGCCACAGAGTGCAGGGCTCCAGTCTCAAG 155
 QY 1510 AGGGGGGTGGCGGCGCATCCGCCCTCGCCCGGGGCGCTGCTGCTCAAGTGGCGGACA 1569
 Db 156 ATGGTCAATGGTACGAGGCAAGTACGTGGCCGACGCACTATGCTCCATATCGGCGATC 215
 QY 1570 CTTTCAGGCGCTCTCCACGCGCAGGTACCGAGCTGCTCCACGCGCGCTGCTCAACA 1629
 Db 216 AGATCGAGATTTTCAGCAACAGGGGCGATACAAAGCGGTGCTGCACCGTACGAGGTGAACA 275

RESULT 10
 US-09-938-842A-2672
 ; Sequence 2672, Application US/09938842A
 ; Patent No. US20020160378A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Harper, Jeff
 ; APPLICANT: Kreps, Joel
 ; APPLICANT: Wang, Xun
 ; APPLICANT: Zhu, Tong
 ; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
 ; FILE REFERENCE: SAME, AND METHODS OF USE
 ; CURRENT APPLICATION NUMBER: US/09/938,842A
 ; PRIOR FILING DATE: 2001-08-24
 ; PRIOR APPLICATION NUMBER: US 60/227,866
 ; PRIOR FILING DATE: 2000-08-24
 ; PRIOR APPLICATION NUMBER: US 60/264,647
 ; PRIOR FILING DATE: 2001-01-16
 ; PRIOR APPLICATION NUMBER: US 60/300,111
 ; PRIOR FILING DATE: 2001-06-22
 ; NUMBER OF SEQ ID NOS: 5379
 ; SEQ ID NO 2672
 ; LENGTH: 1050
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 ; US-09-938-842A-2672

Query Match 2.9%; Score 73.2; DB 9; Length 1050;
 Best Local Similarity 50.9%; Pred. No. 2.3e-09;
 Matches 174; Conservative 0; Mismatches 168; Indels 0; Gaps 0;

QY 1382 CATGGCGCTCACTACTACCGGCTGCCAGAGCCACTCGACACGCTGGCGCACCGGTCC 1441
 Db 600 CATGGCGTTAACTACTATCGCGCTGTCACAGAACCGGAGCTAACTTACGAGCTTCCCGG 659
 QY 1442 GCACCTGGACCCACCTCGCTCACCATCTCCACAGGACCGCTGGCGGCTGGAGGT 1501
 Db 660 ACATAAGACCCACCGCTTATCAGTCTCTTTCAGAGCAAGTCTCTGGTTTGCAGT 719
 QY 1502 GTGGCGGAGGGCGGTGCGCGCCATCGCGCTCGCGCGGCGCTGCTGCAACGT 1561
 Db 720 CTTTAAGAGTAAATAGTGGTGCCTGTAGTCCAAATTCACACACTTTCATGTCATAT 779
 QY 1562 CGCGCACACTTTCATGCGGCTCTCCACGCGAGTACCGAGCTGCTGCGACCGGCGGT 1621
 Db 780 CGCGGACCAATGTCAGGTATAGCAATGATAAATACAGAGTGTGCTCCATAGAGCGGT 839
 QY 1622 CGTCAACAGCAGCGCGCTCGCGGCTCGCTGCGCTTCTTCTGCGCGAGATGGACAC 1681
 Db 840 AGTAARACCGAGAACGAGCGGTATTCGATTCGAGCTTTCTATTTCCCTTCACAGATGC 899
 QY 1682 GTGGTGGCGCGCGGAGGAGTGTGTCGAGCACCCACCC 1723
 Db 900 ACTGATTGTTCCACGACACAGAGTGTGTCATGACAGACTC 941

RESULT 11
 US-09-761-20699
 ; Sequence 20699, Application US/09864761

Patent No. US20020048763A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Penn, Sharon G.
 ; APPLICANT: Rank, David R.
 ; APPLICANT: Hanzel, David K.
 ; APPLICANT: Chen, Wensheng
 ; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL F
 ; FILE REFERENCE: Aecmca-X-1
 ; CURRENT APPLICATION NUMBER: US/09/864,761
 ; CURRENT FILING DATE: 2001-05-23
 ; PRIOR APPLICATION NUMBER: US 60/180,312
 ; PRIOR FILING DATE: 2000-02-04
 ; PRIOR APPLICATION NUMBER: US 60/207,456
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: US 09/632,366
 ; PRIOR FILING DATE: 2000-08-03
 ; PRIOR APPLICATION NUMBER: GB 24263.5
 ; PRIOR FILING DATE: 2000-10-04
 ; PRIOR APPLICATION NUMBER: US 60/236,359
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: PCT/US01/00666
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00667
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00664
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00669
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00665
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00668
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00663
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00662
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00661
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00670
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: US 60/234,687
 ; PRIOR FILING DATE: 2000-09-21
 ; PRIOR APPLICATION NUMBER: US 09/608,408
 ; PRIOR FILING DATE: 2000-08-30
 ; PRIOR APPLICATION NUMBER: US 09/774,203
 ; PRIOR FILING DATE: 2001-01-29
 ; NUMBER OF SEQ ID NOS: 49117
 ; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
 ; SEQ ID NO 20699
 ; LENGTH: 446
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: MAP TO AC007249.2
 ; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 10
 ; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 14
 ; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 13
 ; OTHER INFORMATION: EXPRESSED IN HELI00, SIGNAL = 12
 ; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 13
 ; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 13
 ; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 12
 ; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 13
 ; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 12
 ; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 9.7
 ; OTHER INFORMATION: NT HIT: AL161539.2, EVALUATE 3.70e+00
 ; US-09-864-761-20699

Query Match 2.9%; Score 73; DB 10; Length 446;
 Best Local Similarity 50.7%; Pred. No. 1.5e-09;
 Matches 175; Conservative 0; Mismatches 170; Indels 0; Gaps 0;

QY 738 CAATTAATGACATGTGTGTCGACGAGGAGGTGTGTCGACGCGGCTGCTG 757


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1 // APPLICANT: Penn, Sharon G.
2 // APPLICANT: Rank, David R.
3 // APPLICANT: Hanzel, David K.
4 // APPLICANT: Chen, Wensheng
5 // TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
6 // TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
7 // FILE REFERENCE: Aecmica-X-1
8 // CURRENT APPLICATION NUMBER: US/09/864,761
9 // CURRENT FILING DATE: 2001-05-23
10 // PRIOR APPLICATION NUMBER: US 60/180,312
11 // PRIOR FILING DATE: 2000-02-04
12 // PRIOR APPLICATION NUMBER: US 60/207,456
13 // PRIOR FILING DATE: 2000-05-26
14 // PRIOR APPLICATION NUMBER: US 09/632,366
15 // PRIOR FILING DATE: 2000-08-03
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28 // PRIOR APPLICATION NUMBER: PCT/US01/00665
29 // PRIOR FILING DATE: 2001-01-30
30 // PRIOR APPLICATION NUMBER: PCT/US01/00668
31 // PRIOR FILING DATE: 2001-01-30
32 // PRIOR APPLICATION NUMBER: PCT/US01/00663
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45 // PRIOR FILING DATE: 2001-01-29
46 // NUMBER OF SEQ ID NOS: 49117
47 // SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
48 // SEQ ID NO 2513
49 // LENGTH: 1403
50 // TYPE: DNA
51 // ORGANISM: Homo sapiens
52 // FEATURE:
53 // OTHER INFORMATION: MAP TO AL078472.1
54 // OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 27
55 // OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 19
56 // OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 34
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58 // OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 28
59 // OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 43
60 // OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 20
61 // OTHER INFORMATION: EXPRESSED IN HEL100, SIGNAL = 25
62 // OTHER INFORMATION: EXPRESSED IN HEAT, SIGNAL = 18
63 // OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 21
64 // US-09-864-761-2513

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Query Match 2.9%; Score 71.6; DB 10; Length 1403;
Best Local Similarity 45.2%; Pred. No. 7.7e-09;
Matches 263; Conservative 0; Mismatches 319; Indels 0; Gaps 0;

QY	751	TGGTGTGCACGAGGACGAGAGTGCTGTCGACGGCGGTGCTGACGGGGCAGCG	810
Db	431	TGGTGATGGTGGTGATCGTGCTGGTGGTAGTGGTAGCTGCATGGCTGTTGGTGGTGG	490

[illegible]

Query Match 2.9%; Score 71.4; DB 10; Length 1030;
Best Local Similarity 50.9%; Pred. No. 7.1e-09;
Matches 196; Conservative 0; Mismatches 186; Indels 3; Gaps 1;

Qy	1382	CATCGCGCTCAACTACTACTACCGCGCGTGCACAGAGCCACTGCACACGCTTGGCCACCGCTCC	1441
Db	615	CTTGCAAATTGAACCTCTTACCGCACTTGTCCGATCCGGATCGGGCCATCGGTCTTGGCCGC	674
Qy	1442	GGACTCGGACCCCACTCGCTTCAACATCTCCACAGGACCAAGCTCGCGCGGCTCGGAGGT	1501

Db	675	CCACACCGACTCCACCCCTTCTCACAAATCCCTTTACCAAAACAAACATAAGCGGGTTGACAGT	734
Qy	1502	GT---GGCGGGAGGGCGGTGGCGCCCATCCGCGCCCTCGCCCGGGCGCTCGTGTGCA	1558
Db	735	TCACCGAAAAGCGCGGGTGGGTGACGGTGGCACACAGTCCCGAAGGGCTTTGATCAA	794
Qy	1559	CGTCGGGGACACCTTCATCGGCGCTCTCCACACGCCAGGTACCGCAGCTGCCGACCGGGC	1618
Db	795	TGTAGCGACCTCCCTCCACATATTTGCGAACGGGTTGTACCGGATGTGTCACCGGGT	854
Qy	1619	GGTCGTCACACAGCGCGGCGCTCGCGCTCGCTGGCTTCTTCCTCGCCCGGAGATGA	1678
Db	855	CTTAGTGAAACCGGATCCAGCAAGGCTTCAGTGGGTATTTATGTGGGCCCTCCGAA	914
Qy	1679	CACGGTGGTCGCGCCCGCGGAGGAGTGTGCGACGACCACCCAGGGGTGACCCGGA	1738
Db	915	TGTGGAGATATCTCCACATCGAAGCTAGTGGGCCCAATAAGCTCCCTTTATAAGC	974
Qy	1739	CTTCAGGTGGCGGGCGCTGCTGGAC	1763
Db	975	AGTCACTTGAATGAGTACCTTGGC	999
RESULT 15			
US-09-969-852-4			
; Sequence 4, Application US/09969852			
; Patent No. US20020137211A1			
; GENERAL INFORMATION:			
; APPLICANT: Liu, Tianyan			
; APPLICANT: Liu, Huifen			
; APPLICANT: Li, Wei			
; APPLICANT: Zhao, Libin			
; TITLE OF INVENTION: A METHOD FOR ESTABLISHING AN EXPRESSION SYSTEM OF SPIDER DRAGLINE			
; FILE REFERENCE: LIDU-65			
; CURRENT APPLICATION NUMBER: US/09/969,852			
; PRIOR FILING DATE: 2001-10-04			
; PRIOR APPLICATION NUMBER: CN01106406.4			
; PRIOR FILING DATE: 2001-01-02			
; NUMBER OF SEQ ID NOS: 14			
; SOFTWARE: PatentIn version 3.1			
; SEQ ID NO 4			
; LENGTH: 1852			
; TYPE: DNA			
; ORGANISM: Nephila clavipes			
US-09-969-852-4			
Query Match 2.9%; Score 71.4; DB 10; Length 1852;			
Best Local Similarity 46.5%; Pred. No. 1e-08;			
Matches 271; Conservative 0; Mismatches 306; Indels 6; Gaps 1;			
Qy	761	GCAGGACGAGGAGTGTTCGACGCGGGGTGCTGACGGGGACAGCGAGATCCCGTC	820
Db	151	GCTGGAGGAGGAGTATAGGTGCAAGAGTGCAGGTGCAGCAGCAGCAGCAGCGCTGGA	210
Qy	821	GCAGTTCATATATCCCGGGAGAGAGCCCGGGTGGTGGCGGTGGAGGAGCTGGAGGT	880
Db	211	GCTTCGGACAGGAGGACTAGTGGACAGGTCTGGACAGGAGCTGGAGCAGCGCT	270
Qy	881	GGCGCTGATCGAGTGGGGGGGGGGAGAGTGTGTCGGTGGTCCGCGAGGTGGGGGA	940
Db	271	GCAGCAGCTGGTGGCGGACAGGAGGATATGGAGTCTCGGAAGCCAAAGGTGCAGGA	330
Qy	941	GGCTGGCGAGGACGCGCTTCTTCTGGTGTACCAAGCCATCGAGGGGGCGGTGCT	1000
Db	331	CGAGTGGATCAGTGGGACAGGGCAGGTGCAGCAGCAGCAGCAGCTGGAGGTGCCGA	390
Qy	1001	GGAGGAGCGCACCGGTGCATGAGCGCTCTTT-----CACGCTCCGCTGGGGGAGAA	1054
Db	391	CAAGGAGGATATGGAGTCTTGGAGGCCAAGGTCCAGGACGAGGTGGATTAGTGGACAA	450
Qy	1055	GCAGGGGGCGCAGCGCGCGGGGAGAGCTGCGGCTACGCCACGACGCTTCACGGGGCG	1114

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Db	451	GGTGCAGGTGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGT	510
Qy	1115	CTTCGGCTCCAAAGCTGCCGTGGAAGGAGACGCTGTCTCGGTACTCATTCGGCTGGAGA	1174
Db	511	CTTGTGGACAAAGGTGCCGACAAAGGTGGCTATGGAGGACTTGGAAAGCCAAAGTCCCGGA	570
Qy	1175	TGAAGAGGCGAGGAGGCGCTGGGTGAGTACCTGTCGGGAAGCTCGGGCGGAGCACGG	1234
Db	571	CGAGGAGGATTAGGTGGACAAAGGTGCAGGTGCAGCAGCAGCAGCAGCAGCTGGAGGTGCC	630
Qy	1235	GCGGCGGTGGCGGAGGTGTACTCGCGCTACTGCCACAGAGATGAGCCGCTGTCTCGTGG	1294
Db	631	GGACAGGAGGAGTGTGGACAAAGGTGTGGACAAAGGCTGGAGCAGCCCTGCACGA	690
Qy	1295	GCTGATGAGAGTGTTCGGGGAGAGCCCTGGGCATCTGTGGAGAC	1337
Db	691	GCTGTGTTGTCGGGACAAAGGAGGATATGGAGTCTTTGGAAGCC	733

GenCore version 5.1.4.p5.4578
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Gapop 10.0 , Gapext 1.0
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and is derived by analysis of the total score distribution.

SUMMARIES

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c 2	2033.2	40.7	207376	2	AC104433	AC104433 Oryza sat
c 3	938.8	18.8	207376	2	AC104433	AC104433 Oryza sat
c 4	315.2	6.3	131487	2	AP004117	AP004117 Oryza sat
c 5	274.8	5.5	159290	2	AP004813	AP004813 Oryza sat
c 6	263	5.3	96360	2	AP003867	AP003867 Oryza sat
c 7	263	5.3	134787	2	AP005490	AP005490 Oryza sat
c 8	261.4	5.2	127498	2	AP004759	AP004759 Oryza sat
c 9	231.8	4.6	145999	2	AC096690	AC096690 Oryza sat
c 10	231	4.6	121752	2	AP004130	AP004130 Oryza sat
c 11	231	4.6	176224	2	AP005163	AP005163 Oryza sat
c 12	217.8	4.4	152835	8	AP004224	AP004224 Oryza sat
c 13	216.6	4.3	163704	2	AP004849	AP004849 Oryza sat
c 14	215.8	4.3	126637	2	AC118980	AC118980 Oryza sat
c 15	215.4	4.3	138906	2	AP003946	AP003946 Oryza sat
c 16	215.4	4.3	143160	2	AP004796	AP004796 Oryza sat
c 17	215.4	4.3	148272	2	AP004156	AP004156 Oryza sat
c 18	215.4	4.3	169000	2	AP004991	AP004991 Oryza sat
c 19	215	4.3	121996	2	AP003952	AP003952 Oryza sat
c 20	213.4	4.3	148533	2	AP005449	AP005449 Oryza sat
c 21	213.4	4.3	172368	2	AP003712	AP003712 Oryza sat
c 22	213.4	4.3	175743	2	AP003579	AP003579 Oryza sat
c 23	213	4.3	178959	2	AP004809	AP004809 Oryza sat
c 24	211.4	4.2	111333	2	AC120534	AC120534 Oryza sat
c 25	210.2	4.2	151997	2	OSJN01010	AL607102 Oryza sat
c 26	210.2	4.2	156266	8	AP002542	AP002542 Oryza sat
c 27	209.6	4.2	131768	2	AP005476	AP005476 Oryza sat
c 28	208.4	4.2	142544	2	OSJN00286	AL731641 Oryza sat
c 29	208.2	4.2	172386	2	OSJN00223	AL731585 Oryza sat
c 30	208	4.2	151343	2	AP005003	AP005003 Oryza sat
c 31	207.6	4.2	143515	8	AP003252	AP003252 Oryza sat
c 32	205.8	4.1	124047	2	AC112209	AC112209 Oryza sat
c 33	205.2	4.1	144583	8	AP003262	AP003262 Oryza sat
c 34	205.2	4.1	160925	8	AP004332	AP004332 Oryza sat
c 35	204.2	4.1	114184	2	AP003984	AP003984 Oryza sat
c 36	204.2	4.1	153428	2	AP005535	AP005535 Oryza sat
c 37	203	4.1	176580	2	AP003634	AP003634 Oryza sat
c 38	202.6	4.1	130263	8	OSJN00065	AL606620 Oryza sat
c 39	202.4	4.0	114062	2	OSJN00267	AL731619 Oryza sat
c 40	202	4.0	176349	8	AP002092	AP002092 Oryza sat
c 41	201.6	4.0	137152	2	AP004564	AP004564 Oryza sat
c 42	201.6	4.0	171970	2	AP004764	AP004764 Oryza sat
c 43	201.4	4.0	159420	2	AP005459	AP005459 Oryza sat
c 44	199.8	4.0	145739	8	OSJN00157	AL682937 Oryza sat
c 45	199.6	4.0	122882	2	AC093088	AC093088 Oryza sat

ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION
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PROGRESS ***
AC096690
AC096690.4 GI:20503077
HTG; HTGS_PHASE2.
ORYZA SATIVA.
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1 (bases 1 to 145999)
AUTHORS
Buell,C.R., Yuan,Q., Ouyang,S., Liu,J., Tallon,L., Gansberger,K.,

Db 77519 TTTCTCCGCGCAATTCGCCAATCTACAGTCCCTGCTACTGATCTCTCTCCCTACCGGTGAG 77460
QY 3661 CTGGTCCCCACCATTTCAACTCTCAAGCAACATTCACCCCATCAATCCCGTAATCTCGC 3720
Db 77459 CTGGTCCCCACCATTTCAACTCTCAAGCAACATTCACCCCATCAATCCCGTAATCTCGC 77400
QY 3721 CCGCGTGGCCCAATTTGCGTCAAGCTCTCCAGCGCGCCCTCCAGGAATTCACGC 3780
Db 77399 CCGCGTGGCCCAATTTGCGTCAAGCTCTCCAGCGCGCCCTCCAGGAATTCACGC 77340
QY 3781 TCGGTCAACATCGTCTCTCCCGCGCCAAACCCCTTCTCTCAACAGCGGATGGCTGGCCAG 3840
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Db 77219 GATGCTGCTTTGATCTGGATCGCTCGGGACCGGAGACAGCAAGCAATGTCATGTT 77160
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Db 76139 GTCCCGCGGAGTGGCGCCCG 76119

RESULT 2
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LOCUS
DEFINITION
AC104433
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
JOURNAL
REFERENCE
AUTHORS
JOURNAL
COMMENT

AC104433 207376 bp DNA linear HTG 02-APR-2002
Oryza sativa chromosome 3 clone OJ1754_E06, *** SEQUENCING IN PROGRESS ***
AC104433 31-19111667
HTG: HTGS_PHASE1.
Oryza sativa.
Oryza sativa
Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta: Spermatophyta: Magnoliophyta: Liliopsida: Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
Buell, R.
Submitted (11-DEC-2001) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA
Buell, R.
Submitted (02-APR-2002) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA
On Mar 5, 2002 this sequence version replaced gi:18767486.
* NOTE: this is a 'working draft' sequence. It currently consists of 34 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
* 10102: contig of 10102 bp in length
* 10151: gap of unknown length
* 10152: contig of 2954 bp in length
* 13106: gap of unknown length
* 13154: contig of 7386 bp in length
* 20540: gap of unknown length
* 20541: contig of 2393 bp in length
* 22983: gap of unknown length
* 23032: contig of 2611 bp in length

*	25643	25691:	gap of unknown length
*	25692	31250:	contig of 5559 bp in length
*	31251	31299:	gap of unknown length
*	31300	34474:	contig of 3175 bp in length
*	34475	34523:	gap of unknown length
*	34524	37120:	contig of 2597 bp in length
*	37121	37169:	gap of unknown length
*	37170	39229:	contig of 2060 bp in length
*	39230	39278:	gap of unknown length
*	39279	41558:	contig of 2280 bp in length
*	41559	41607:	gap of unknown length
*	41608	47008:	contig of 5401 bp in length
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*	47058	49299:	contig of 2242 bp in length
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*	52195	70888:	contig of 18694 bp in length
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*	181045	185204:	contig of 4160 bp in length
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*	185253	195354:	contig of 10102 bp in length
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BASE COUNT			
ORIGIN			
Query Match 40.7%; Score 2033.2; DB 2; Length			
Best Local Similarity 94.88; Pred. No. 0;			
Matches 205; Conservative 0; Mismatches 111; Indels			

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QY	2435	CCGTCGATAATCACTTTATACCAAGTCAAGAATGACTTTGGCTATGCACAAATGAACAGGAGCA	2494
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RESULT 3	
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DEFINITION	AC104433 207376 bp DNA linear HTG 02-APR-2002
ACCESSION	AC104433.3 GI:19111667
VERSION	HTG; HTGS_PHASE1.
KEYWORDS	ORYZA SATIVA
SOURCE	ORYZA SATIVA
ORGANISM	ORYZA SATIVA
REFERENCE	Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaceae; Oryza.
AUTHORS	Buell,C.R., Yuan,Q., Ouyang,S., Liu,J., Tallon,L., Gansberger,K., Kim,M., Overton II,L., Bera,J., Tsitrin,T., Krol,M., Jarrahi,B., Jin,S., Koo,H., Zismann,V., Hsiao,J., Blunt,S., Vanaken,S., Utterbach,T., Feldblyum,T., Yang,Q., Haas,B., Suh,B., Peterson,J., Quackenbush,J., White,O., Salzberg,S. and Fraser,C.
TITLE	Oryza sativa ssp. japonica cv. Nipponbare OJ1754_E06 BAC genomic
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 207376)
AUTHORS	Buell,R.
TITLE	Direct Submission
JOURNAL	Submitted (11-DEC-2001) The Institute for Genomic Research, 9712
REFERENCE	Medical Center Dr. Rockville, MD 20850, USA
AUTHORS	3 (bases 1 to 207376)
TITLE	Buell,R.
JOURNAL	Direct Submission
COMMENT	Submitted (02-APR-2002) The Institute for Genomic Research, 9712 Medical Center Dr. Rockville, MD 20850, USA On Mar 5, 2002 this sequence version replaced gi:18767486. * NOTE: this is a 'working draft' sequence. It currently * consists of 34 contigs. The true order of the pieces * is not known and their order in this sequence record is * arbitrary. Gaps between the contigs are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence * as soon as it is available and the accession number will * be preserved. * * 1 10102: contig of 10102 bp in length * 10103 10151: gap of unknown length * 10152 13105: contig of 2954 bp in length * 13106 13154: gap of unknown length * 13155 20540: contig of 7386 bp in length * 20541 20589: gap of unknown length * 20590 22982: contig of 2393 bp in length * 22983 23031: gap of unknown length * 23032 25642: contig of 2611 bp in length * 25643 25691: gap of unknown length * 25692 31250: contig of 5559 bp in length * 31251 31299: gap of unknown length * 31300 34474: contig of 3175 bp in length * 34475 34523: gap of unknown length * 34524 37120: contig of 2597 bp in length * 37121 37169: gap of unknown length * 37170 39229: contig of 2060 bp in length * 39230 39278: gap of unknown length * 39279 41558: contig of 2280 bp in length * 41559 41607: gap of unknown length * 41608 47008: contig of 5401 bp in length * 47009 47057: gap of unknown length * 47058 49299: contig of 2242 bp in length * 49300 49348: gap of unknown length * 49349 52145: contig of 2797 bp in length * 52146 52194: gap of unknown length * 52195 70888: contig of 18694 bp in length * 70889 70937: gap of unknown length * 70938 82563: contig of 11626 bp in length

Df 134194 -----AGTTGGGAGGCACBAGGTGGAGGATCGAGAGAATCAGTTCGAGAAAGG 134246

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RESULT 8
AP004759
LOCUS 127498 bp DNA linear HTG 21-MAR-2002
DEFINITION Oryza sativa (japonica cultivar-group) chromosome 8 clone P0670E08.
*** SEQUENCING IN PROGRESS ***, in ordered pieces.

ACCESSION AP004759
VERSION AP004759.1 GI:18656405
KEYWORDS HTG; HTGS_PHASE2.
SOURCE Oryza sativa (japonica cultivar-group) (cultivar:Nipponbare) DNA,
clone:P0670E08.

ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Eriarthroideae; Orzyeae; Oryza.

REFERENCE 1
AUTHORS Sasaki,T., Matsumoto,T. and Yamamoto,K.
TITLE Oryza sativa nipponbare(G83) genomic DNA, chromosome 8, PAC
clone:P0670E08
JOURNAL Published Only in Database (2002)
REFERENCE 2 (bases 1 to 127498)
AUTHORS Sasaki,T., Matsumoto,T. and Yamamoto,K.
TITLE Direct Submission
JOURNAL Submitted (13-FEB-2002) Takuji Sasaki, National Institute of
Agrobiological Sciences, Rice Genome Research Program; Kanondai
2-1-2, Tsukuba, Ibaraki 305-8602, Japan
(E-mail:tsasakienias.afric.go.jp, URL:http://rtp.dna.afrc.go.jp/,
Tel:81-298-38-7441, Fax:81-298-38-7468)

COMMENT NOTE: It currently consists of 1 contigs. Gaps between the contigs
are represented as runs of N. The order of the pieces is believed
to be correct as given, however the sizes of the gaps between them
are based on estimates that have provided by the submitter. This
sequence will be replaced by the finished sequence as soon as it is
available and the accession number will be preserved.
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

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 /cultivar="Nipponbare"
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ORIGIN

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Matches 468; Conservative 0; Mismatches 161; Indels 50; Gaps 6

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Db 77026 ACTATGCGCTGATCTTGGTATCAGCTGTGATATCTTCGACGTTTCACACGTGATATCGA 77085

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PROGRESS ***, 5 ordered pieces.
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VERSION AC096690.4 GI:20503077
KEYWORDS HTG; HTGS.PHASE2.
SOURCE Oryza sativa.
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 14599)
Buell, C.R., Yuan, Q., Ouyang, S., Liu, J., Tallon, L., Cansberger, K.,
Kim, M., Overton II, L., Bera, J., Tsitrin, T., Krol, M., Jarrahi, B.,
Jin, S., Koo, H., Zismann, V., Hsiao, J., Blunt, S., Vanaken, S.,
Uterbach, R., Feldblyum, T., Yang, Q., Haas, B., Suh, B., Peterson, J.,
Quackenbush, J., White, O., Salzberg, S. and Fraser, C.
Oryza sativa ssp. japonica cv. Nipponbare OSJNBa0059G06 BAC genomic
sequence
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 14599)
AUTHORS Buell, R.
TITLE Direct Submission
JOURNAL
SUBMITTED (22-SEP-2001) The Institute for Genomic Research, 9712
MEDICAL CENTER DR, ROCKVILLE, MD 20850, USA
3 (bases 1 to 14599)
Buell, R.
TITLE Direct Submission
JOURNAL
SUBMITTED (08-MAY-2002) The Institute for Genomic Research, 9712
MEDICAL CENTER DR, ROCKVILLE, MD 20850, USA
ON MAY 6, 2002 this sequence version replaced gi:19881803.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 5 contigs. Gaps between the contigs

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* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
*
* 1 3902: contig of 3902 bp in length
* 3903 4002: gap of unknown length
* 4003 71267: contig of 67265 bp in length
* 71268 71367: gap of unknown length
* 71368 94679: contig of 23312 bp in length
* 94680 94779: gap of unknown length
* 94780 122220: contig of 27441 bp in length
* 122221 122320: gap of unknown length
* 122321 145999: contig of 23679 bp in length.
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* Location/Qualifiers
* 1..145999
* /organism="Oryza sativa"
* /cultivar="Nipponbare"
* /db_xref="taxon:4530"
* /chromosome="3"
* /clone="OSJNBa0059G06"
* /note="japonica cultivar-group"
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BASE COUNT 40847 a 32003 c 31335 g 41412 t 402 others
ORIGIN

Query Match 4.6%; Score 231.8; DB 2; Length 145999;
Best Local Similarity 64.7%; Pred. No. 1.8e-28;
Matches 385; Conservative 0; Mismatches 192; Indels 18; Gaps 2;

QY 1183 ACCTGGATGAGGAGAGGTGGCATGCGGAGATCGCGCGCAGGTTGCGGACGAGCATG 1242
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 75694 ACCTGGATACACAGAGCTCCCGCAACCCAGTCTCCCGCAGCTCGCGGACGACCATGCC 75753
QY 1243 GCCATCCCGCGGCGTACTGTTGGCTCGGCCCGCAGCAGCAGCTGTCCCTCTCCCTCTGG 1302
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 75754 TCCATCTCCGCGGCTACACCTCCGCTCCCGCGGATGTTCCGCTCTCCCTCTGG 75813
QY 1303 TACCAGAGGACAGCGCGATGCGG-----CCGCGCGTCTCGAGGCGCAGC 1347
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 75814 TACCACAGCAGCGCGCCCATCTCGCCCTGCACCTGCACCGCGCGTGGCCATGCGCGCC 75873
QY 1348 CTGGAGCGCGGACGAGATCGGATAGAGTCTGCTTGGCCCTTGGCCCGAGTCGCGCATCTG 1407
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 75874 CTGGCGCGCGCCACCATCGCTCGTACAGCTCCGCTCCCTCTGTCAGTTGGCATGGGC 75933
QY 1408 GTGCGCGCGCAGCGCGAGGAGCGCGGATGACAGGAA---CTGGCGCGGAGCGAAGG 1464
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 75934 GTGCTCCCTGGCGGAGGAGCGGCGGATGACGGTGGAGGCGGATGCGCGGAAG 75993
QY 1465 AGGCGGTAGCGAGGACATCCCGGACCGGACGCGCGAGTGGCGGTGGAGTCGATGCCG 1524
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 75994 AGGCGGTGGCGAAGGACATCCCGCGGCGCCACCGCGAGCAGCTGTGGACGTGCGATGCC 76053
QY 1525 TTGTGGAGCGGCTCTGTGGGCTCTCCCATCGAGCTCGCGGAGGAGCGAGGATGGAG 1584
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 76054 CGGTGGAGGGCTCCCGCGCTCTCCACCGGAGCTCAGGGGACACCGAGGATGGGA 76113
QY 1585 GGGTTGGGGCGCATCTCCGGGGGAACCATGCGCTCCAGTTCGAGTGGAGACCCACACGCCGCC 1644
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 76114 GGTGACGGGGCGCATCTCCGGGCGCACCGCGCTCCACCGCGCGTGGTGGCGCGCGC 76173
QY 1645 CGCCCCGCGCATCTGTCAGTTCGCGCTCCAGGATGAACACACCTTGTTCAGCGGAGGAGG 1704
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 76174 CGACCGCGCATGTTGGACTGCGCGCGCCAAAAGGAATATCAGGCTCGGGGTCGCGCGC 76233
QY 1705 GACACAGCGCGCGCGCGCGGAGAGCAGCAGCAGCAGGAGCATCGCGCGCA 1759
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 76234 GTGGCGGTGGCGCGTGTGGCGAGCAGCAGCAGCGCTAGTACCTGCGAGCTGTA 76288

RESULT 10

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AP004130      121752 bp      DNA      linear      HTG 21-MAR-2002
LOCUS      Oryza sativa (japonica cultivar-group) chromosome 8 clone
DEFINITION      OJ1014_B05, *** SEQUENCING IN PROGRESS ***, in ordered pieces.
ACCESSION      AP004130
VERSION      HTG; HTGS_PHASES2.
KEYWORDS
SOURCE
ORGANISM      Oryza sativa (japonica cultivar-group) (cultivar:Nipponbare) DNA,
              clone:OJ1014_B05.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
AUTHORS      Sasaki,T., Matsumoto,T. and Yamamoto,K.
TITLE      Oryza sativa nipponbare(GA3) genomic DNA, chromosome 8, BAC
              clone:OJ1014_B05
JOURNAL      Published Only in Database (2001)
REFERENCE
AUTHORS      Sasaki,T., Matsumoto,T. and Yamamoto,K.
TITLE      Direct Submission
JOURNAL      Submitted (05-SEP-2001) Takuji Sasaki, National Institute of
              Agrobiological Sciences, Rice Genome Research Program; Kannondai
              2-1-2, Tsukuba, Ibaraki 305-8602, Japan
              (E-mail:tsasakienias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/,
              Tel:81-298-38-7441, Fax:81-298-38-7468)
COMMENT      The nucleotide sequence of this BAC clone was generated by
              combining Monsanto and RGP-Japan sequencing data.
              NOTE: It currently consists of 1 contigs. Gaps between the contigs
              are represented as runs of N. The order of the pieces is believed
              to be correct as given, however the sizes of the gaps between them
              are based on estimates that have provided by the submitter. This
              sequence will be replaced by the finished sequence as soon as it is
              available and the accession number will be preserved.
              * NOTE: This is a 'working draft' sequence.
              * This sequence will be replaced
              * by the finished sequence as soon as it is available and
              * the accession number will be preserved.
FEATURES
source
location/Qualifiers
1..121752
   /organism="Oryza sativa (japonica cultivar-group)"
   /cultivar="Nipponbare"
   /db_xref="taxon:39947"
   /chromosome="8"
   /clone="OJ1014_B05"
BASE COUNT      32506 a 27609 c 27315 g 34122 t      200 others
ORIGIN
Query Match      4.6%; Score 231; DB 2; Length 121752;
Best Local Similarity 94.1%; Pred. No. 2.5e-28;
Matches 240; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
QY 4131 TAGTACTCCCTCCGTCCTCAAAAATAAGTGTAGTTTGTAGCATTATTCATGTTCAACGTTTGA 4190
Db 95625 TACTACTCCCTCCGTCCTCAAAAATAAGTGTAGTTTGTAGCATTATTCATGTTCAACGTTTGA 95684
QY 4191 CCATTGCGTCTATTGTGAAAAAGATTATGATTAGTATTTTATTGTTATTAGATGATAAA 4250
Db 95685 CCGTTCGCTCTATTGTGAAAAATATATGATTAGTATTTTGTGTTATTAGATGATAAA 95744
QY 4251 ACATGAATAGTACTTTATGTGTGACTAAATTTTTTTTAAATATTTTATTAAATTTTCAAA 4310
Db 95745 ACATGAATAGTAAATTTATGTGTGACTAAATTTTTTTTAAATATTTTATTAAATTTTCAAA 95804
QY 4311 ATAAGACGGATGGTCAAAAGCGCTAAACATGGATATCTATGCTACATTTATTTTGGGACG 4370
Db 95805 ATAAGACGGATGGTCAAAAGCGCTAAACATGGATATCTATGCTACATTTATTTTGGGACG 95864
QY 4371 GAGGTAGTAGGCTAT 4385
Db 95865 GAGGTAGTAGATTTT 95879

```

```

RESULT 11
LOCUS      AP005163
DEFINITION      Oryza sativa (japonica cultivar-group) chromosome 8 clone
              OSJNBa0053M06, *** SEQUENCING IN PROGRESS ***, in ordered pieces.
ACCESSION      AP005163
VERSION      121752 bp      DNA      linear      HTG 17-MAY-2002
KEYWORDS      OSJNBa0053M06, *** SEQUENCING IN PROGRESS ***, in ordered pieces.
SOURCE      HTG; HTGS_PHASES2.
ORGANISM      Oryza sativa (japonica cultivar-group) (cultivar:Nipponbare) DNA,
              clone:OSJNBa0053M06.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
AUTHORS      Sasaki,T., Matsumoto,T. and Katayose,Y.
TITLE      Oryza sativa nipponbare(GA3) genomic DNA, chromosome 8, BAC
              clone:OSJNBa0053M06
JOURNAL      Published Only in Database (2002)
REFERENCE
AUTHORS      Sasaki,T., Matsumoto,T. and Katayose,Y.
TITLE      Direct Submission
JOURNAL      Submitted (15-MAY-2002) Takuji Sasaki, National Institute of
              Agrobiological Sciences, Rice Genome Research Program; Kannondai
              2-1-2, Tsukuba, Ibaraki 305-8602, Japan
              (E-mail:tsasakienias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/,
              Tel:81-298-38-7441, Fax:81-298-38-7468)
COMMENT      The nucleotide sequence of this BAC clone was generated by
              combining Monsanto and RGP-Japan sequencing data.
              NOTE: It currently consists of 1 contigs. Gaps between the contigs
              are represented as runs of N. The order of the pieces is believed
              to be correct as given, however the sizes of the gaps between them
              are based on estimates that have provided by the submitter. This
              sequence will be replaced by the finished sequence as soon as it is
              available and the accession number will be preserved.
              * NOTE: This is a 'working draft' sequence.
              * This sequence will be replaced
              * by the finished sequence as soon as it is available and
              * the accession number will be preserved.
FEATURES
source
location/Qualifiers
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   /organism="Oryza sativa (japonica cultivar-group)"
   /cultivar="Nipponbare"
   /db_xref="taxon:39947"
   /chromosome="8"
   /clone="OSJNBa0053M06"
BASE COUNT      49574 a 38250 c 38489 g 49729 t      182 others
ORIGIN
Query Match      4.6%; Score 231; DB 2; Length 176224;
Best Local Similarity 94.1%; Pred. No. 2.5e-28;
Matches 240; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
QY 4131 TAGTACTCCCTCCGTCCTCAAAAATAAGTGTAGTTTGTAGCATTATTCATGTTCAACGTTTGA 4190
Db 46774 TACTACTCCCTCCGTCCTCAAAAATAAGTGTAGTTTGTAGCATTATTCATGTTCAACGTTTGA 46833
QY 4191 CCATTGCGTCTATTGTGAAAAAGATTATGATTAGTATTTTATTGTTATTAGATGATAAA 4250
Db 46834 CCGTTCGCTCTATTGTGAAAAATATATGATTAGTATTTTGTGTTATTAGATGATAAA 46893
QY 4251 ACATGAATAGTACTTTATGTGTGACTAAATTTTTTTTAAATATTTTATTAAATTTTCAAA 4310
Db 46894 ACATGAATAGTAAATTTATGTGTGACTAAATTTTTTTTAAATATTTTTCATAAATTTTCAA 46953
QY 4311 ATAAGACGGATGGTCAAAAGCGCTAAACATGGATATCTATGCTACATTTATTTTGGGACG 4370
Db 46954 ATAAGACGGATGGTCAAAAGCGCTAAACATGGATATCTATGCTACATTTATTTTGGGACG 47013
QY 4371 GAGGTAGTAGGCTAT 4385
Db 47014 GAGGTAGTAGATTTT 47028
RESULT 12

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AP004224 152835 bp DNA linear PLN 13-JUL-2002
 LOCUS Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 1,
 DEFINITION BAC clone:B1111E11.
 ACCSSION AP004224.3 GI:21743333
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Oryza sativa (japonica cultivar-group) (cultivar:Nipponbare) DNA,
 clone:B1111E11.
 Oryza sativa (japonica cultivar-group)
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzaceae; Oryza.
 1
 Sasaki,T., Matsumoto,T. and Yamamoto,K.
 Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, BAC
 clone:B1111E11
 Published Only in Database (2001)
 2 (bases 1 to 152835)
 Sasaki,T., Matsumoto,T. and Yamamoto,K.
 Direct Submission
 Submitted (03-OCT-2001) Takuji Sasaki, National Institute of
 Agrobiological Sciences, Rice Genome Research Program; Kannondai
 2-1-2, Tsukuba, Ibaraki 305-8602, Japan
 (E-mail:tsasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/,
 Tel:81-298-38-7441, Fax:81-298-38-7458)
 On Jul 12, 2002 this sequence version replaced gi:17026098.
 Genes were predicted from the integrated results of the following:
 GENSscan1.0, BLASTN2.0, BLASTX2.0 as well as SplicePredictor
 (October 1998 version). The genomic sequence was searched against
 NCBI NonRedundant Protein database, nr
 (ftp://ncbi.nlm.nih.gov/blast/db) and the cDNA sequence database at
 RGP. Protein homologies of the coding regions were searched against
 NCBI NonRedundant Protein database with BLASTP2.0. ESTs represent
 the identified cDNA sequences using BLASTN 2.0 with the
 corresponding DBJ accession no. and RGP clone ID.
 A gene with identity or significant homology to a protein is
 classified based on the protein name to indicate the homology level
 such as same name, 'putative-' and '-like protein'. A gene without
 significant homology to any protein but with EST homology (covering
 almost the entire length of partial sequence) is classified as an
 'unknown' protein. A gene predicted with a gene prediction program
 is classified as a 'hypothetical' protein.
 The orientation of the sequence is from -21M13 to M13-rev of the BAC
 clone. This sequence of B1111E11 clone has an overlap with B1080D07
 (DDAT:AP003203) at the position 146,696 to 152,835 of 3' end.
 Detailed information on overlap and assembly quality together with
 annotation of this entry is available at
 http://rgp.dna.affrc.go.jp/GenomeSeq.html.
 FEATURES
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 1. 152835
 /organism="Oryza sativa (japonica cultivar-group)"
 /cultivar="Nipponbare"
 /db_xref="taxon:39947"
 /chromosome="1"
 /clone="B1111E11"
 /note="3' LTR"
 complement(1..514)
 /note="3' LTR"
 complement(530..6029)
 /gene="B1111E11.1"
 complement(530..6029)
 /gene="B1111E11.1"
 /note="probably inactive due to stop codon(s) in CDS
 pseudogene, polyprotein"
 /pseudo
 Join(8253..8336,8386..8595)
 /gene="B1111E11.2"
 Join(8253..8336,8386..8595)
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 /note="hypothetical protein"
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 /db_xref="GI:21743334"

/translation="MTSPPAVARAKLASERRRDDANGGHOHNGRRRRGRNGNLR
 LDDGGAPATVGGGVGDIQGLVTTATSPNSDDRDITDGGARLKRRRRR"
 complement(8839..9352)
 /note="5' LTR"
 complement(Join(14589..14792,14904..15023,15078..15290,
 15389..15607,15720..15865,16296..16365))
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 /codon_start=1
 /product="putative annexin"
 /protein_id="BAC03328.1"
 /db_xref="GI:21743335"
 /translation="MEDHTRKLNQKADTASAEVHKSGGWGDEQAVIGVLAHRDATOR
 KQIRLTETENYENLQRLQSELGDLERHWHVLPDVERQAVWNTATKCIHEDFA
 VVIRIACNTSSSELAVKETYHYKYKLSLEDVAARATNLRLSLALVYRVDGE
 VNDALAKSEAKILHETVNTGDHGLIRIVGTRSAQNLNATFSWFRDERGTSITKIH
 APRFDQALQHGADPTGYSHALTRCISDANKYFVKLRNMAHKSGTNEDSLTRVI
 VLHAEKDLGIGKDAFOKRAVALEKAIQNTDTSQDKSELMALIGSI"
 complement(Join(17303..17441,21169..21190,21797..22025,
 22151..22324))
 /gene="B1111E11.4"
 complement(Join(17303..17441,21169..21190,21797..22025,
 22151..22324))
 /gene="B1111E11.4"
 /note="hypothetical protein"
 /codon_start=1
 /protein_id="BAC03329.1"
 /db_xref="GI:21743336"
 /translation="WVYIMDSIRLINKYKRHKOVORNFRLDITMIDIIKVIIRM
 KNTVKTSLILGVGILLINSYSGEICVCKYKETHPAYKETHLRPIRKYTDWRA
 HKSGDTAEWIVIVAIRANOSVSLPKERGLDSEVDGLSNKNPMLEKINLADLHQ
 WNAVHIFTIRINITEINAGKRIYVSG"
 Join(24567..24773,24885..25163,25427..25524,25675..25882)
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 Join(24567..24773,24885..25163,25427..25524,25675..25882)
 /gene="B1111E11.5"
 /note="hypothetical protein
 similar to Oryza sativa chromosome10, OSJNBb0089F16.9"
 /codon_start=1
 /protein_id="BAC03330.1"
 /db_xref="GI:21743337"
 /translation="MTGFNLSENFKENPEAFRSVRPVVAPKSLPIEKLAIPVPT
 EKTWASTLEFPAAPSADNVAFLOFLICSTYTIKGNLDAYRLRLEFSLGRAKQ
 WFTYRVAVNTWKCTAFSLRFPFPGKINALRGRISSFOOTKDESLPEAWERLQEIIG
 KWTIEBGRAGGTRETRNRRERSSSSVOMSGVPPSPSESSSSSSRWDLSEI
 IRRMDTLDIQIGIQLNLTETHVAQTQEWQQAQAFANINDMMQQ"
 30135..32223
 /gene="B1111E11.6"
 30135..32223
 /gene="B1111E11.6"
 /note="probably inactive due to stop codon(s) in CDS
 pseudogene, retroelement"
 /pseudo
 Join(35262..35643,43596..43702)
 /gene="B1111E11.7"
 Join(35262..35643,43596..43702)
 /gene="B1111E11.7"
 /note="hypothetical protein"
 /codon_start=1
 /protein_id="BAC03331.1"
 /db_xref="GI:21743338"
 /translation="MFLTGKVKVRQRMIFGHIGVGCVRGKNSIRSHGELFSINA
 NIGTGCDFVRNOKAKPKHDFTWYWSLRAFAVTHFVIRAAFNLCOLIATAHGG
 AMFFDRNEKVQKAPKQDFWTYWSVKERTAFETFGDDEPREFENLRNDRSYAKHTSKAT
 SL"
 Join(44530..44843,44934..45375)
 /gene="B1111E11.8"
 Join(44530..44843,44934..45375)
 /gene="B1111E11.8"
 /note="hypothetical protein
 similar to Oryza sativa chromosome3, OSJNBa0026A15.9"

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WPGSGDATHWEHASGLRAKRRRRWRDCEAEEGGDVSHRTGEAAQAAGWPA
PRKEVEVGRGAAPENLGGKLENNARGFHIGEERELATGEANGTGGGIGARRWK
VAGVGAGVDDMGHSRGLGGTEEGMINSF"
complement(46012..46653)
/gene="B1111E11.9"
CDS
complement(46012..46653)
/gene="B1111E11.9"
/notes="hypothetical protein
similar to Oryza sativa chromosome10, OSJNB0089F16.9"
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/protein_id="BAC03333.1"
/db_xref="GI:21743340"
/translation="MTGNLPENFKPEPAFRGVRPAVAPQKLTPEKPAIPAPI
FNMASKTLREFAEDSTNVAIGPQINIGMDPDLKSLITMAQASFCGKPNVDANA
HLQAFLEICSTVTIKGVSPOAIRLFPFSLIGRAKQFVYANRAVNTWKCPGLS
KFPFMKTNALGRISNFOQTRDESIPREALRLQEVAAACPHGMDDWLIVTS"
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CDS
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/db_xref="GI:21743341"
/translation="MRALPEKYELVTMLNSDMRMTPTASLLGKINTNDMKLKK
EMEAASFSPKUKIRAK"
53847..54335
LTR
/notes="5' LTR"
55770..57616
gene
/notes="B1111E11.11"
55770..57616
misc_feature
/notes="B1111E11.11"
/notes="probably inactive due to stop codon(s) in CDS
pseudogene, retroelement"
57629..58116
LTR
/notes="3' LTR"
join(60720..61097,61272..61421,62316..62685,62854..62971,
63077..63192,63282..63374,63454..63549,64125..64847,
64968..65116,66390..66476,66497..66581)
/gene="B1111E11.12"
CDS
join(60720..61097,61272..61421,62316..62685,62854..62971,
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64968..65116,66390..66476,66497..66581)
/gene="B1111E11.12"
/notes="hypothetical protein
similar to Arabidopsis thaliana chromosome 3, At3g54500"
/codon_start=1
/protein_id="BAC03335.1"
/db_xref="GI:21743342"

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Query Match 4.4%; Score 217.8; DB 8; Length 152835;
Best Local Similarity 86.8%; Pred. No. 4e-26;
Matches 252; Conservative 0; Mismatches 37; Indels 2; Gaps 1;

QY 4129 AATAGTACTCCCTCGCTCAAAATAGTGTAGTATTAGCACTATTTCATGTTCAACGTTT 4188
DB 78155 AAGACTACTCCCTCGCTCCCAAAATAGTGTAGTATTAGCACTATTTCATGTTCAACGTTT 78214

QY 4189 GACCATTCGCTTATTGAAAAGATATGATTAGTATTATTTTATTGTTATTAGATGATA 4248
DB 78215 GACCGTTCATCTTATTGAAAAGATATGATTAGTATTATTTTATTGTTATTAGATGATA 78274

QY 4249 AACATGATAGTACTTTATGCTGTGACTAAATTTTTTTTAAATATTTTATTATTAATTTTC 4308
DB 78275 AACATGATAGTACTTTATGCTGTGACAAA--TTTTTTAAATATTTTTCATAAATTTTC 78332

QY 4309 AAATAAGCGGATGTCACAAAGCGCTAAACATGATATCTATGCGTACACATTTATTGGGA 4368

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|||||
Db 78333 AAATAGCGGATGGCTCAAAAGCGCTAAACAGGATATCTAGCTCCACTTATTTTGGGA 78392
|||||
QY 4369 CGGAGTAGTAGGCTATATAACACAGCTATATAACATATTTTAAAGAGATAAAA 4419
|||||
Db 78393 CGGAGTAGTATACCTTAGTCCCAACCAATAAGATCTAACTTATCGAA 78443
|||||

RESULT 13
AP004849/c 163704 bp DNA linear HTG 23-MAR-2002
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) chromosome 2 clone
OJ1311.D08, ** SEQUENCING IN PROGRESS ***, in ordered pieces.
ACCESSION
AP004849
VERSION
AP004849.1 GI:19698269
KEYWORDS
HTG; HTGS_PHASE2.
SOURCE
Oryza sativa (japonica cultivar-group) (cultivar:Nipponbare) DNA,
clone:OJ1311.D08.
ORGANISM
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1
Sasaki, T., Matsumoto, T. and Yamamoto, K.
Oryza sativa nipponbare(GA3) genomic DNA, chromosome 2, BAC
clone:OJ1311.D08
JOURNAL
Published Only in Database (2002)
REFERENCE
2 (bases 1 to 163704)
Sasaki, T., Matsumoto, T. and Yamamoto, K.
Direct Submission
JOURNAL
Submitted (20-MAR-2002) Takuji Sasaki, National Institute of
Agrobiological Sciences, Rice Genome Research Program; Kannondai
2-1-2, Tsukuba, Ibaraki 305-8602, Japan
(E-mail:tsasaki@nias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/,
Tel:81-298-38-7441, Fax:81-298-38-7468)
COMMENT
The nucleotide sequence of this BAC clone was generated by
combining Monsanto and RGP-Japan sequencing data.
NOTE: it currently consists of 1 contigs. Gaps between the contigs
are represented as runs of N. The order of the pieces is believed
to be correct as given, however the sizes of the gaps between them
are based on estimates that have provided by the submitter. This
sequence will be replaced by the finished sequence as soon as it is
available and the accession number will be preserved.
* NOTE: this is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
FEATURES
Location/Qualifiers
source
1..163704
/organism="Oryza sativa (japonica cultivar-group)"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/chromosomes="2"
/clone="OJ1311.D08"
BASE COUNT 46733 a 35204 c 34892 g 46875 t
ORIGIN

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Query Match 4.3%; Score 216.6; DB 2; Length 163704;
Best Local Similarity 92.0%; Pred. No. 6.3e-26;
Matches 240; Conservative 0; Mismatches 19; Indels 2; Gaps 1;

QY 4129 AATAGTACTCCCTCGCTCAAAATAGTGTAGTATTAGCACTATTTCATGTTCAACGTTT 4188
DB 77913 ACTGTACTCCCTCGCTCCCAAAATAGTGTAGTATTAGCACTATTTCATGTTTACATT 77954

QY 4189 GACCATTCGCTTATTGAAAAGATATGATTAGTATTATTTTATTGTTATTAGATGATA 4248
DB 77953 GACCGTTCGCTTATTGAAAAGATATGATTAGTATTATTTTATTGTTATTAGATGATA 77794

QY 4249 AACATGATAGTACTTTATGCTGTGACTAAATTTTTTTTAAATATTTTATTATTAATTTTC 4308
DB 77793 AACATGATAGTACTTTATGCTGTGACTAA--TTTTTTTAAATATTTTTCATAAATTTTC 77736

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QY 4309 AATAAGACGGATGCTCAAGCGCTAAACATGGATATCTATGCTACACTTATTTGGGA 4368
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DB 77735 AATFAGACGGATGCTCAAGCGCTAAATATGGATATCTATGCTACACTTATTTGGGA 77676
|||||

QY 4369 CGGAGGTAGTATGTTCCCAAC 4389
|||||
DB 77675 CGGAGGTAGTATGTTCCCAAC 77655
|||||

RESULT 14
AC118980 126637 bp DNA linear HTG 23-APR-2002
LOCUS Oryza sativa chromosome 3 clone OJ1263H11, *** SEQUENCING IN
DEFINITION PROGRESS ***, 3 ordered pieces.
ACCESSION AC118980
VERSION AC118980.1 GI:20270052
KEYWORDS HTG; HTGS_PHASE2.
SOURCE Oryza sativa.
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE Wang,R.A., Yu,Y., Soderlund,C., Chen,M., Kim,H.-R., Rambo,T.,
AUTHORS Saski,C., Henry,D., Oates,R. and Simmons,J.
TITLE Rice Genomic Sequence
JOURNAL Unpublished
REFERENCE 2. (bases 1 to 126637)
AUTHORS Wang,R.A., Yu,Y., Soderlund,C., Chen,M., Kim,H.-R., Rambo,T.,
Saski,C., Henry,D., Oates,R. and Simmons,J.
TITLE Direct Submission
JOURNAL Submitted (23-APR-2002) Clemson University Genomics Institute,
Clemson University, 100 Jordan Hall, Clemson, SC 29634, USA
COMMENT * NOTE: This is a 'working draft' sequence. It currently
* consists of 3 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 1 19607: contig of 19607 bp in length
* 19608 90592: contig of 70985 bp in length
* 90593 126637: gap of unknown length in length.
* 126637: contig of 36045 bp in length.
FEATURES
Location/Qualifiers
1. 126637
/organism="Oryza sativa"
/db_xref="taxon:4530"
/chromosome="3"
/clone="OJ1263H11"
BASE COUNT 36868 a 27250 g 35263 t 5 others
ORIGIN
Query Match 4.3%; Score 215.8; DB 2; Length 126637;
Best Local Similarity 94.4%; Pred. No. 8.4e-26;
Matches 235; Conservative 0; Mismatches 12; Indels 2; Gaps 1;

QY 4131 TAGTACTCCCTCCGCTCAAAATAAGTGTAGTTTACGACTATTCATGTTCAACGTTTGA 4190
|||||
DB 113552 TAGTACTCCCTCCGCTCAAAATAAGTGTAGTTTACGACTATTCATGTTCAACGTTTGA 113611
|||||

QY 4191 CCATTCGCTCTATTGAAAAGATATGATAGTAGTATTATTGTTATGATAGATATAA 4250
|||||
DB 113612 CCGTTCGCTCTATTGAAAAGATATGATAGTAGTATTATTGTTATGATAGATATAA 113671
|||||

QY 4251 ACATGATAGTACTTATGTCGCACTAATTTTTTTTAAATATTTTATTAATTTTCAA 4310
|||||
DB 113672 AATGATAGTACTTATGTCGCACTAATTTTTTTTAAATATTTTATTAATTTTCAA 113729
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QY 4311 AFAAGACGGATGCTCAAGCGCTAAACATGGATATCTATGCTACACTTATTTGGGACG 4370
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DB 113730 ATAAGACGGATGCTCAAGCGCTAAATACGATATTTATGCTGCTATTTGGGACG 113789
|||||
QY 4371 GAGGTAGTA 4379
|||||
DB 113790 GAGGTAGTA 113798
|||||

RESULT 15
AP003946 138906 bp DNA linear HTG 21-MAR-2002
LOCUS Oryza sativa (japonica cultivar-group) chromosome 6 clone
DEFINITION OJ1147.D11, *** SEQUENCING IN PROGRESS ***, in ordered pieces.
ACCESSION AP003946
VERSION AP003946.1 GI:15021916
KEYWORDS HTG; HTGS_PHASE2.
SOURCE Oryza sativa (japonica cultivar-group) (cultivar:Nipponbare) DNA,
clone:OJ1147.D11.
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1.
AUTHORS Sasaki,T., Matsumoto,T. and Yamamoto,K.
TITLE Oryza sativa nipponbare(GA3) genomic DNA, chromosome 6, BAC
clone:OJ1147.D11
JOURNAL Published Only in Database (2001)
REFERENCE 2. (bases 1 to 138906)
AUTHORS Sasaki,T., Matsumoto,T. and Yamamoto,K.
TITLE Direct Submission
JOURNAL Submitted (25-JUL-2001) Takuji Sasaki, National Institute of
Agrobiological Resources, Rice Genome Research Program; Kannondai
2-1-2, Tsukuba, Ibaraki 305-8602, Japan
(B-mail:tsasakienias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/,
Tel:81-298-38-7441, Fax:81-298-38-7468)
COMMENT The nucleotide sequence of this BAC clone was generated by
combining Monsanto and RGP-Japan sequencing data.
NOTE: It currently consists of 1 contigs. Gaps between the contigs
are represented as runs of N. The order of the pieces is believed
to be correct as given, however the sizes of the gaps between them
are based on estimates that have provided by the submitter. This
sequence will be replaced by the finished sequence as soon as it is
available and the accession number will be preserved.
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 1. 138906
Location/Qualifiers
/organism="Oryza sativa (japonica cultivar-group)"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/chromosome="6"
/clone="OJ1147.D11"
BASE COUNT 39967 a 29996 c 29997 g 38791 t 155 others
ORIGIN
Query Match 4.3%; Score 215.4; DB 2; Length 138906;
Best Local Similarity 91.3%; Pred. No. 9.9e-26;
Matches 240; Conservative 0; Mismatches 21; Indels 2; Gaps 1;

QY 4117 AAGACGAGGTAGTACTCCCTCCGCTCAAAATAAGTGTAGTTTACGACTATTTCA 4176
|||||
DB 11539 AGGGGAAGAAACAAGTACTCCCTCCGCTCAAAATAAGTGTAGTTTACGACTATTTCA 11598
|||||

QY 4177 TGTTCAACGTTTGACCATTCGCTTTATTGTTGAAAAGATATGATAGTATTTTATGT 4236
|||||
DB 11599 TGTTCAACGTTTGACCGTTCGCTTTATTGTTGAAAAGATATGATAGTATTTTATGT 11658
|||||

QY 4237 TATTAGATGATAAAACATCAATGACTTTTATGCTGCTACTATTTTAAATATTTT 4296
|||||
DB 11659 TATTAGATGATAAAACATCAATGACTTTTATGCTGCTACTATTTTAAATATTTT 11716
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GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

Run on: March 25, 2003, 18:27:39 ; Search time 762.288 Seconds
(without alignments)
14774.266 Million cell updates/sec

Title: US-09-702-134-7212_COPY_62300_67300

Perfect score: 5001
Sequence: 1 aggggaactaacttcca.....tgcgcggagtgcccccg 5001

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_101002.*

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23: /SID32/gcgdata/geneseq/geneseq-emb1/NA2001B.DAT.*
24: /SID32/gcgdata/geneseq/geneseq-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	139.8	2.8	561	24 ABL49988	Rice Ditto-Os1 nuc
2	139.8	2.8	561	24 ABL49989	Rice Ditto-Os1 nuc
3	137.4	2.7	5113	21 AA261434	Nucleotide sequenc
4	129.8	2.6	544	24 ABL49987	Rice Ditto-Os1 nuc
5	121.8	2.4	5757	21 AA261433	Nucleotide sequenc
c 6	118.8	2.4	2943	21 AAC48061	Arabidopsis thalia
7	118.4	2.4	949	24 ABN98574	Arabidopsis thalia
c 8	118.4	2.4	1024	24 AAC45528	Arabidopsis thalia
c 9	118.4	2.4	3108	21 AAC46278	Arabidopsis thalia

c 10	118.4	2.4	3187	21 AAC47620	Arabidopsis thalia
c 11	117.8	2.4	1024	21 AAC4895	Arabidopsis thalia
c 12	114.4	2.3	547	21 AAX79573	Pinus radiata cell
c 13	107.8	2.2	2380	20 AAX32000	Rice pyruvate deca
c 14	107.8	2.2	5526	20 AAX31999	Rice pyruvate deca
c 15	99	2.0	15686	24 AAD38801	Rice RGA38 contig.
c 16	94.4	1.9	5579	24 AAL46958	Rice lesion inhibi
c 17	91.6	1.8	1730	24 AAI72980	OSGRP-Al full leng
c 18	91.6	1.8	3572	24 AAI72979	OSGRP-Al coding se
c 19	89.6	1.8	267	24 ABL49990	Rice Ditto-Os2 nuc
c 20	84.2	1.7	312	24 ABL49992	Rice Ditto-Os2 nuc
c 21	83.4	1.7	246	24 ABL49991	Rice Ditto-Os2 nuc
c 22	75.6	1.5	500	24 AAI72978	OSGRP-Al larger pr
c 23	73.2	1.5	1026	20 AAX3542	Rice beta-glucanas
c 24	73.2	1.5	2169	20 AAX3534	Rice beta-glucanas
c 25	69.6	1.4	91552	24 AAD38803	BAC clone KGP36 fr
c 26	65.4	1.3	18155	24 AAD38808	CODR4 ORF from ric
c 27	65.4	1.3	91552	24 AAD38803	BAC clone KGP36 fr
c 28	64.6	1.3	4569	24 ABK15663	Rice lipoxigenase
c 29	62.8	1.3	1993	21 AAA63731	DNA encoding a pol
c 30	62.4	1.2	58857	21 AAA58471	Nucleotide sequenc
c 31	62	1.2	1806	21 AAA50102	Human ztr2 consen
c 32	62	1.2	12120	24 AAS96695	Rice DMF1 DNA. Or
c 33	62	1.2	125401	22 AAD17186	Streptomyces nous
c 34	61.6	1.2	65140	22 AAD17184	Streptomyces nous
c 35	61.2	1.2	1050	22 AAD21685	Mutational hot spo
c 36	61.2	1.2	2849	22 AAD21684	Human retinitis pi
c 37	61	1.2	863	24 ABK77958	Bacillus clausii g
c 38	61	1.2	4403765	22 AAI99683	Mycobacterium tube
c 39	61	1.2	4411529	22 AAI99682	Mycobacterium tube
c 40	60.6	1.2	1280	21 ABQ62495	Mycobacterium bovi
c 41	60.6	1.2	15872	18 AAF68715	Streptomyces venez
c 42	60.6	1.2	15872	21 AA287283	S. venezuelae vep
c 43	60.4	1.2	1591	18 AAT93780	Oryza sativa patho
c 44	60	1.2	390	13 AAQ21833	Randomising oligon
c 45	60	1.2	390	14 AAQ36859	PCR primer for 5'

ALIGNMENTS

RESULT 1
ABL49988
ID ABL49988 standard; DNA; 561 BP.
AC ABL49988;
XX
DT 10-JUN-2002 (first entry)
XX
DE Rice Ditto-Os1 nucleotide sequence SEQ ID NO:63.
XX
KW Rice; plant; detection; polymorphism; transposable element; genome;
KW gene; ds.
XX
OS Oryza sativa.
XX
PN WO200212484-A1.
XX
PD 14-FEB-2002.
XX
PF 02-AUG-2001; 2001WO-JP066661.
XX
PR 02-AUG-2000; 2000JP-0234577.
XX
PA (NLSB) JAPAN TOBACCO INC.
PA (SYGN) SYNGENTA LTD.
XX
PI Komori T, Nitta N;
XX
DR WPI; 2002-241759/29.
XX
PT Construction of marker for detecting plant genome polymorphism with use of transposable element, useful particularly in studying restriction


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FT      /**tag= b
FT      ./number= 1
FT      1592..3056
FT      /**tag= c
FT      /number= 1
FT      3057..4898
FT      /**tag= d
FT      /number= 2
XX
XX      WO200008162-A1.
XX      PN
XX      PN
XX      XX
XX      PD
XX      PD
XX      PD
XX      XX
XX      03-AUG-1999; 99WO-US17706.
XX      XX
XX      04-AUG-1998; 98US-0095229.
XX      21-JUN-1999; 99US-0336946.
XX      XX
XX      (DUPO ) DU PONT DE NEMOURS & CO E. I.
XX      Valent BS, Bryan GT;
XX      PI
XX      PI
XX      WPI; 2000-205715/18.
XX      DR
XX      P-PSDB; AAY69308.
XX      DR

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Query Match	2.7%;	Score 137.4;	DB 21;	Length 5113;
Best Local Similarity	85.5%;	Pred. No. 3.2e-19;		
Matches 165;	Conservative 0;	Mismatches 26;	Indels 2;	Gaps 1;
QY 4375	TAGTAGGCTATAAACACAGCTATAAACATATTTAAAGAGATAAAGAGAGAGAGAAATAG	4434		
Db 2630	TAGCAGGTTATAGCTTAGCTATAACATATTTAAAGATATAGAGAGAGAGAGAG	2689		
QY 4435	CAGCGGACTATATATTTGTAGCCAGCTACAGCAGGACTCAAGACGTAAATGTGTATA	4494		
Db 2690	CAGCAGCCTACAGATCTGTAGCCAGCTGCAGCAGGACTCTAAGACGTAAATGTG--TA	2747		
QY 4495	TCGCAAGTAGGACGACGATTTAAGAGTATAGTAGCAACTATTGTATCAATTAAGCTATTA	4554		
Db 2748	TCAGCAGTAGGACCGAGTATTATATAGTATAGTAGAGCACTATTGTATGGAATGGCTATT	2807		
QY 4555	CATTAACTATGAT	4567		
Db 2808	GGCTCTAGATGAT	2820		

RESULT 4	
ABL49987	
ID	ABL49987 standard; DNA; 544 bp.
XX	
XX	
XX	ABL49987;
XX	
DT	10-JUN-2002 (first entry)
XX	
XX	
DE	Rice Ditto-Osl nucleotide sequence SEQ ID NO:62.
XX	

KW	Rice; plant; detection; polymorphism; transposable element; genome;
KW	gene; ds.
OS	Oryza sativa.
PN	WO200212484-A1.
XP	14-FEB-2002.
PD	
PP	02-AUG-2001; 2001WO-JP06661.
PF	
XX	02-AUG-2000; 2000JP-0234577.
PR	(NISR) JAPAN TOBACCO INC.
PA	(SYGN) SYNGENTA LTD.
PI	Komori T, Nitta N;
PP	WIPI; 2002-241759/29.
DR	
XX	
PT	Construction of marker for detecting plant genome polymorphism with use
PT	of transposable element, useful particularly in studying restriction
PT	fragment length polymorphism applicable in cell genetics -
XX	
PS	Example 4; Fig 17; 110pp; Japanese.
XX	
CC	The present invention describes a method for constructing a marker for
CC	detecting polymorphisms in a plant genome. The method comprises the
CC	production of a primer for nucleic acid amplification by using the base
CC	sequences of a transposable element and/or the domain adjacent to it.
CC	Also described is a marker for detection polymorphisms in plant genomes
CC	The constructed marker can be used for detecting plant genome
CC	polymorphisms, which is useful particularly in studying restriction
CC	fragment length polymorphism applicable in cell genetics e.g. for
CC	analysing and selecting specific breeds of plants. The method is simple,
CC	easy, less time consuming and not so laborious, e.g. in the study of
CC	less frequently occurring polymorphism between various species to enable
CC	identification of the site and isolation of the required gene.
CC	ABL49926 to ABL50036 represent nucleotide sequences used in the
CC	exemplification of the present invention.
XX	
SQ	Sequence 544 BP; 179 A; 72 C; 91 G; 202 T; 0 other;
Query Match	2.6%; Score 129.8; DB 24; Length 544;
Best Local Similarity	74.9%; Pred No. 5.5e-18;
Matches 176; Conservative	0; Mismatches 57; Indels 2; Gaps
QY	4385 TAAACCAGCTATAAACAATATTTTAAAGAGATAAAAGAAGAGAGATAATGCACGGACTA 4444
Db	34 TAAGTCAGCTATAAACATATTTTAAAGAGATAAAAAAGATAGAGAAGACGCGGCTA 93
QY	4445 TATATTTCAGCAGCTACAGCACGGACTCAAGACGTAATGTCTGTATATGACACAGTAG 4504
Db	94 CAGATCTGTAGTCAGCTCAGACCGGACTTCAATAGCTGAATGTATG--TAGTATAGGTGG 151
QY	4505 GACCAAGGTATTATAGATAGTAAAGCAACTATTGTATGAATTAGCTATTACATTAACACT 4564
Db	152 GACCAAGTATTATATAGTACAGTAGCAACTATTGTATGAATTGACTATTACATTGGCTAT 211
QY	4565 GATGATTTGAGCGCGCTCTAAOCAGCGGTATATATTTTTATTTGAGCCAATCCTCFCA 4619
Db	212 AGATGATTTTAAAGTATAGTATGGGTACTACTATTAACTTGCTCTTAATTCGTTTGA 266

XX	Disease resistance protein; rice; variety Yashiro-mochi; Pi-ta gene;
KW	resistance gene; Pi-ta resistance gene-mediated defence response;
XN	fungal pathogen; rice blast fungus; ss.
XX	Oryza sativa.
FF	Key Location/Qualifiers
FT	CDS 1256..5505
FT	/tag= a
FT	/product=
FT	/note= "contains 1 intron"
FT	exon 1256..2200
FT	/tag= b
FT	intron /number= 1
FT	2201..3663
FT	/tag= c
FT	exon /number= 1
FT	3664..5505
FT	/tag= d
FT	/number= 2
XX	WO200008162-A1.
PX	17-FEB-2000.
XX	03-AUG-1999; 99WO-US17706.
PF	PR 98US-0095229.
PPR	21-JUN-1999; 99US-0336946.
XX	(DUPO) DU PONT DE NEMOURS & CO E I.
XX	Valent BS, Bryan GT;
PI	WIPI; 2000-205715/18.
DR	p-PADB; AAY69307.
XX	Noval nucleic acid fragments conferring Pi-ta resistance gene-mediated
PT	defence response for producing transgenic plants resistant to fungal
PT	pathogens, especially rice blast fungus -
PS	Claim 1; Page 56-57; 96pp; English.
CC	The present sequence encodes a disease resistance protein of rice
CC	variety Yashiro-mochi. The rice pi-ta gene was cloned by a map-based
CC	cloning strategy. The pi-ta protein has a novel structure, compared
CC	to all known classes of resistance gene products. The polynucleotide
CC	sequence confers a pi-ta resistance gene-mediated defence response
CC	against diseases caused by fungal pathogens, particularly the rice
CC	blast fungus. Introduction of the cloned pi-ta gene into susceptible
CC	rice confers resistance to pathogen strains.
XX	
SQ	Sequence 5757 BP; 1638 A; 1202 C; 1251 G; 1666 T; 0 other;
Query Match	2.4%; Score 121.8; DB 21; Length 5757;
Best Local Similarity	86.0%; Pred. No. 7.5e-16;
Matches 147; Conservative	0; Mismatches 22; Indels 2; Gaps
QY	4397 AAACATATTTTAAAGAGATAAAGAAGAGAGAGAATAAGCAGCGGACTATATATTCTTACC 4456
DB	3259 AAAACATATTTTAAAGAGATATAGGAAGAGAGAGAGAGAGAGCACTACAGATCTGTACC 3318
QY	4457 CAGCTACAGCAGGGCTCAAGACGTAATGTGTATATGACAAGTAGGCAGGTATTA 4516
DB	3319 CAGCTGCAGCACGGACTTCAGACGTAATGTGTG--TATGACAGTGAGGCCAAGTATTA 3376
QY	4517 AGAGTATAGTAAGCAACTATTGTGTAATGAATTAGCTATTACATTAACATATCAT 4567
DB	3377 ATAGTATAGTAAGCAACTATTGTGTAATGAATTGCTATTGGCTCTAGATGAT 3427
RESULT	6

PR	23-AUG-1999;	99US-0149902;
PR	23-AUG-1999;	99US-0149930;
PR	25-AUG-1999;	99US-0150566;
PR	26-AUG-1999;	99US-0150884;
PR	27-AUG-1999;	99US-0151065;
PR	27-AUG-1999;	99US-0151066;
PR	27-AUG-1999;	99US-0151080;
PR	30-AUG-1999;	99US-0151303;
PR	31-AUG-1999;	99US-0151438;
PR	01-SEP-1999;	99US-0151930;
PR	02-SEP-1999;	99US-0152363;
PR	10-SEP-1999;	99US-0153070;
PR	13-SEP-1999;	99US-0153758;
PR	15-SEP-1999;	99US-0154018;
PR	16-SEP-1999;	99US-0154303;
PR	20-SEP-1999;	99US-0154779;
PR	22-SEP-1999;	99US-0155139;
PR	23-SEP-1999;	99US-0155486;
PR	24-SEP-1999;	99US-0155659;
PR	28-SEP-1999;	99US-0156458;
PR	29-SEP-1999;	99US-0156596;
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PR	05-OCT-1999;	99US-0157753;
PR	06-OCT-1999;	99US-0157865;
PR	07-OCT-1999;	99US-0158232;
PR	08-OCT-1999;	99US-0158369;
PR	12-OCT-1999;	99US-0159293;
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PR	13-OCT-1999;	99US-0159295;
PR	13-OCT-1999;	99US-0159329;
PR	14-OCT-1999;	99US-0159330;
PR	14-OCT-1999;	99US-0159331;
PR	14-OCT-1999;	99US-0159637;
PR	14-OCT-1999;	99US-0160814;
PR	18-OCT-1999;	99US-0159584;
PR	21-OCT-1999;	99US-0160741;
PR	21-OCT-1999;	99US-0160767;
PR	21-OCT-1999;	99US-0160768;
PR	21-OCT-1999;	99US-0160770;
PR	21-OCT-1999;	99US-0160814;
PR	21-OCT-1999;	99US-0160815;
PR	22-OCT-1999;	99US-0160980;
PR	22-OCT-1999;	99US-0160981;
PR	22-OCT-1999;	99US-0160989;
PR	25-OCT-1999;	99US-0161404;
PR	25-OCT-1999;	99US-0161405;
PR	25-OCT-1999;	99US-0161406;
PR	26-OCT-1999;	99US-0161359;
PR	26-OCT-1999;	99US-0161360;
PR	26-OCT-1999;	99US-0161361;
PR	28-OCT-1999;	99US-0161920;
PR	28-OCT-1999;	99US-0161992;
PR	28-OCT-1999;	99US-0161993;
PR	29-OCT-1999;	99US-0162142;
PR	29-OCT-1999;	99US-0162143;

Best Local Similarity 55.8%; Pred. No. 2.5e-15

Qy	1181	ATACCTGGATGACGAGAGAGCTGTGCATCGGCGACAGATCGCGCGAGGTTCGGGACGACGCA	1240
Db	2920	AGACCTGAATTAATGGGAGAGAGAGAGGTTGAGATCATGACGAGAGTTCCTTAATCAAC	2861
Qy	1241	TGGCCATCCGGCGGGCGTACTCCGTTGGCGTGGCCGACGACGAGTGCCTCTCCGCCCT	1300
Db	2860	GATCCATATTGTTGCCCGTAGCTCTCGGGCGTATGGATGTCCACACGTCATCTCTCTCCT	2801
Qy	1301	GGTACCAAGAGACGCGCGATGGCGCGCGGTCTCGAGGCGGACCTCGAGCGCGGCA	1360
Db	2800	GATACCAACACCGCGCTTGTATCTCGCGCGCATTTCTTCTACTCTCCCTCCGTTCTCTTGA	2741
Qy	1361	CGAGATCGGAGTAGAGGTGCGTCCCTTTGGGCCACAGTCGCGCCATCTGGTGGCGCGCGAGG	1420

Db 2740 CCATCTCTCTGTACAGTGGCTCCACGCTCCCACTCTTTATGCGCGTCCACCGGAAG 2681
 QY 1421 CGCAGGGGAGAGCGCGATGACAGGAAGTGGCCGGAGCGAAG-----GAGGGGGTTAG 1474
 Db 2680 CGCAGCGGACCAACCGATCACAGCGAATCGTTTCCAGGCGATCTTCCACCGGTTAG 2621
 QY 1475 CGAAGGACATCCCGGAGCGACCGCCGAGGTGCGGTTGGAGTCGATGCGGTGTGGACGG 1534
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 QY 1535 GTCGTGGGCTCTCTCCATCGAGTGGGGGAGAGCGGAGATGAGGGGTGGGGG 1594
 Db 2560 GTCGTGTGCTTCTCCACCGGAGATCGGACAGCGAGGATCGATGATTTGTTG 2501
 QY 1595 CGCACTCCGGGGACCATCGCTCCCA 1622
 Db 2500 CGCATTCGGTGAAGGATTTATCCCA 2473

RESULT 7

ABN98574
 ID ABN98574 standard; DNA; 949 BP.
 XX AC ABN98574;
 XX DT 01-AUG-2002 (first entry)
 XX DE Arabidopsis thaliana expressed polynucleotide SEQ ID NO 342.
 XX KW Arabidopsis thaliana; plant; insecticide; fungicide; transgenic; stress;
 XX KW disease; crop; thale cress; tolerance factor; insect; pathogen;
 XX KW nutrition; ds.
 XX OS Arabidopsis thaliana.
 XX PN US200203281-A1.
 XX PD 21-FEB-2002.
 XX PF 26-JAN-2001; 2001US-0770445.
 XX PR 27-JAN-2000; 2000US-178472P.

(GOREL/) GORLACH J.
 (ANYI/) AN Y.
 (HAMIL/) HAMILTON C M.
 (PRIC/) PRICE J L.
 (RAIN/) RAINES T M.
 (YUYI/) YU Y.
 (RAME/) RAMEKA J G.
 (PAGE/) PAGE A.
 (MATH/) MATHAW A V.
 (LEDF/) LEDFORD B L.
 (WOBES/) WOESSNER J P.
 (HAAS/) HAAS W D.
 (GARC/) GARCIA C A.
 (KRICK/) KRICKER M.
 (SLAT/) SLATER T.
 (DAVI/) DAVIS K R.
 (ALLE/) ALLEN K.
 (HOFF/) HOFFMAN N.
 (HURB/) HURBAN P.

Gorlach J, An Y, Hamilton CM, Price JL, Raines TM, Yu Y,
 Rameka JG, Page A, Mathew AV, Ledford BL, Woessner JP, Haas WD;
 Garcia CA, Kricker M, Slater T, Davis KR, Allen K, Hoffman N;
 Hurban P;
 WPI; 2002-400781/43.
 New Arabidopsis thaliana nucleic acid for identifying homologous genes,
 producing compositions that modulate the expression or function of its

PT encoded protein, and mapping functional regions of protein -
 XX Claim 1; SEQ ID NO 342; 49pp + Sequence Listing; English.
 XX The invention relates to an Arabidopsis thaliana nucleic acid (I)
 CC comprising a sequence capable of hybridizing under stringent conditions
 CC to a sequence selected from any one of 999 sequences (ABN98233-ABN99231),
 CC given in the specification or its fragment. A polypeptide (II) encoded by
 CC (I), a transgenic plant (III) comprising an exogenous nucleic acid or a
 CC genetically modified cell (IV) comprising an exogenous nucleic acid, is
 CC useful for screening a candidate agent for its biological effect. (I) is
 CC useful in identifying homologous or related genes, in producing
 CC compositions that modulate the expression or function of its encoded
 CC protein, mapping functional regions of the protein and in studying
 CC associated physiological pathways. (I) is also useful for the genetic
 CC manipulation of cells, particularly plant cells. (I) is also useful in
 CC screening assays of various plant strains to determine the strains that
 CC are best capable of withstanding a particular disease or environmental
 CC stress. (II) and (III) are useful for screening of biologically active
 CC agents, e.g. fungicides, insecticides, etc., for elucidating biochemical
 CC pathways. The screened agents are useful in improved methods of treating
 CC crops to prevent or treat disease. (II) are also useful in screening
 CC programs to identify agents that mimic or enhance the action of tolerance
 CC factors. Such agents are useful in improved methods of treating crops to
 CC enhance their tolerance to environmental stress. (I) is also useful
 CC for enhancing or inhibiting production of a biosynthetic product in a
 CC plant. (III) is useful for identifying other mediators that may induce
 CC expression of proteins of interest, for establishing the extent to which
 CC any specific insect and/or pathogen is responsible for damage to a
 CC particular plant, for identifying other mediators that enhance or induce
 CC tolerance to environmental stress, for identifying factors involved in
 CC biosynthetic pathways of nutritional, commercial, or medicinal value and
 CC for identifying productions of nutritional, commercial or medicinal
 CC value. (IV) is useful in the study of genetic function and regulation,
 CC for alteration of the cellular metabolism and for screening compounds,
 CC that may affect the biological function of the gene or gene products.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from USPTO
 CC at seqdata.uspto.gov/sequence.html?DocID=99990970445.

XX Sequence 949 BP; 227 A; 248 C; 198 G; 276 T; 0 other;

Query Match 2.4%; Score 118.4; DB 24; Length 949;
 Best Local Similarity 55.8%; Pred. No. 1.9e-15;
 Matches 249; Conservative 0; Mismatches 191; Indels 6; Gaps 1;

QY 1183 ACCTGATGAGGAGAGGTGTGTGGCGATGCGGCGAGGTTCGGACGAGCATG 1242
 Db 400 ACCTGANTATGGGAGAGAGAGAGGTGTGAGATCATGACGGAGGTCTTAATCAACGA 459
 QY 1243 GGCATCCGGCGGGCTACTCGTTGGCGTCGGCCCGACGAGGTGTGCTTCCCCCTGG 1302
 Db 460 TCCATATTGTTCCCGTAGCTCTCGGGTTCATGGATGTCCACACGCTCACTCTCTCTGA 519
 QY 1303 TACCAGAGGACAGCGCGATGCGGCGCGGTCTCGAGGGCGACCTTGGAGCGGGGACG 1362
 Db 520 TACCACAAACACCGCTTGAFTCTCTCGCGCGCATTTCTCTCTCTCTCTCTGACC 579
 QY 1363 AGATCGGAGTAGAGTCTGTCGCTTGGCCGATGCGGCATCTGTCGCGCGCGCGCG 1422
 Db 580 ATCTCTCTGTACAGTGGCTTCCACGCTCCACACTTTTATGCGCGGTTCACCGGAACGG 639
 QY 1423 CAGGGGACGAGCGCGATGACAGGGAATCGCCGGAGCGAAG-----GAGGGCGTTAGCG 1476
 Db 640 CACGGCACCAACCGATCACAGCGGAATCTGTTCCAGGCGATTTTTCACCGCGTTAGCG 699
 QY 1477 AAGGACATCCGGAGCCGACGCGCGAGTGTGAGTCGATGCGGTGTGGAGCGGC 1536
 Db 700 AAGGCCATTTCTTGGACCTACTCCACACACTTTTACCTGTGTCAATGTCAACGTGTAGTGGC 759
 QY 1537 TCGTGGGCTCTCTCCATCGAGTCTCGGGGAGAGCGGAGGATGGAGGGTTGGGGCG 1596
 Db 760 TCGTGTGCTTCTTCCCGGAGATCTCGGAGACGCGGAGGATCGATGAGTTTGTGCG 819

QY 1597 CACTCCGGGGGAACCATGCGTCGCCA 1622
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Db 820 CACTCCGGTGGAGAGATTATCCCA 845

RESULT 8
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ID AAC45528 standard; DNA; 1024 BP.
XX AAC45528;
XX AC AAC45528;
XX DT 18-OCT-2000 (first entry)
XX DE Arabidopsis thaliana DNA fragment SEQ ID NO: 46825.
XX KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX OS Arabidopsis thaliana.
XX PN EP1033405-A2.
XX PD
XX PF 06-SEP-2000.
XX PF 25-FEB-2000; 2000EP-0301439.
XX PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
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PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
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PR 01-SEP-1999; 99US-0151930.
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PR	25-OCT-1999;	99US-0161404.	PR	25-OCT-1999;	99US-0161405.
PR	25-OCT-1999;	99US-0161406.	PR	25-OCT-1999;	99US-0161406.
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PR	28-OCT-1999;	99US-0161920.	PR	28-OCT-1999;	99US-0161920.
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PR	28-OCT-1999;	99US-0161993.	PR	28-OCT-1999;	99US-0161993.
PR	29-OCT-1999;	99US-0162142.	PR	29-OCT-1999;	99US-0162142.
Query Match 2.4%; Score 118.4; DB 21; Length 3108;					
Best Local Similarity 55.8%; Pred. No. 3.1e-15;					
Matches 249; Conservative 0; Mismatches 191; Indels 6; Gaps 1;					
QY	1183	ACCTGATGAGGAGAGGTGGCAGGAGATCGGCGCAGGTTCGGGACGAGCATG	1242		
Db	2918	ACCTGATGAGGAGAGAGGAGGTTGAGATCATGACGGAGGTTCTTAATCAACGA	2859		
QY	1243	GCCATCGGCGGGGTACTTCGTTGGCTGGCCCGCCAGCGACGTGCTCTCCCTCGG	1302		
Db	2858	TCCATATTGTTCCGCTAGCTCTCGGCGTCATGGATGTCACACACGCTCACTCTCTCTTGA	2799		
QY	1303	TACCAGAGGACAGCGCGATCGGCGCGCGCTCTCGAGGCGCACCTGGAGCGCGGACG	1362		
Db	2798	TACCACAAACCGCGCTGATCTCTCCGCGCATTTCTACTCTCTCTCTCTGACC	2739		
QY	1363	AGATCGGATGAGGTGGTGGCTTGGCCAGTCGGCCGATCTTGGTGCCTCCGCGACGGCG	1422		
Db	2738	ATCCCTCTGTAAGTGGGTTCCAGCTCCCACTCTTTATCGCGCTTCCACCGGAAGCG	2679		
QY	1423	CAGGGACGAGCGCGATGACAGGAATCGGCGGAGCGAAG-----GAGGCGCTTAGCG	1476		
Db	2678	CAGGACACACCGCATGACAGCGAATCTGTTTCCAGCGGATTTCTCACCGCTTAGCG	2619		
QY	1477	AAGGACATCCGCGACCGACCGCGATGCGGTTGGAGTCGATGCCGTTGTGAGCGCGC	1536		
Db	2618	AACGCCATTCCTGGACCTACTCCACACACTTTACCTGTGTCAATGTCAACGTTAGTGC	2559		
QY	1537	TCGTGGGCTCTCCATCGGAGCTGGGCGAGAGCGGAGGATGAGGCTTGGGGCG	1596		
Db	2558	TCGTGTGCTTCTCCACCGGAGATCTCGGACAGCGGAGGATCGATGAGTTGGTGCG	2499		
QY	1597	CATCTCCGGGGAACCATGCGCTGCCA	1622		
Db	2498	CATTCGCGTGAAGGATTTATCCCA	2473		
RESULT 10					
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ID	AAC47620 standard; DNA; 3187 BP.				
XX	AAC47620;				
DT	18-OCT-2000 (first entry)				
XX	Arabidopsis thaliana DNA fragment SEQ ID NO: 54497.				
DE	Arabidopsis thaliana				
XX	Hybridisation assay; genetic mapping; gene expression control;				
KW	protein identification; signal transduction pathway;				
KW	metabolic pathway; promoter; termination sequence; ss.				
XX	Arabidopsis thaliana.				
OS	Arabidopsis thaliana.				
XX	EP1033405-A2.				
PN	06-SEP-2000.				
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XX	25-FEB-2000; 2000EP-0301439.				
XX	25-FEB-1999; 99US-0121825.				
PR	05-MAR-1999; 99US-0123180.				
PR	09-MAR-1999; 99US-0123548.				

PR 16-JUL-1999; 99US-0144085.
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 PR 19-JUL-1999; 99US-0144325.
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 PR 04-OCT-1999; 99US-0157117.
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 PR 25-OCT-1999; 99US-0161404.
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 PR 26-OCT-1999; 99US-0161359.
 PR 26-OCT-1999; 99US-0161360.
 PR 26-OCT-1999; 99US-0161361.
 PR 28-OCT-1999; 99US-0161920.
 PR 28-OCT-1999; 99US-0161992.
 PR 28-OCT-1999; 99US-0161993.
 PR 29-OCT-1999; 99US-0162142.

Query Match 2.4%; Score 118.4; DB 21; Length 3187;
 Best Local Similarity 55.8%; Pred. No. 3.le-15;
 Matches 249; Conservative 0; Mismatches 131; Indels 6; Gaps 1;

OY 1183 ACCTGGATGAGGAGAGGTGTGCATGCGGAGATCGCGCCAGGTGGCGGACGAGCATG 1242
 DB 2997 ACCTGAATATGGAGAGAGAGAGGTGGAGATCATGACGAGGTTCTTAATCAACGA 2938
 OY 1243 GCCATCCGGCGGGCGTACTCGTTGGCGTCGGCCCGACGCGACGCTGCTCTCCCGCTGG 1302
 DB 2937 TCCATATTGTTCCCGTAGCTCTCGGCGTCATGATGATCCACACGCTCACTCTCTCTGA 2878
 OY 1303 TACACAGGACAGCCCGAGTCGGCGCGCGCTCTCGAGGGCGACCCCTGGAGCGCGGACG 1362
 DB 2877 TACCACACACCGCCTTGATCTCTCGCGCGCATTTCCCTACTCTCTCTCTCTCTGACC 2818
 OY 1363 AGATCGGAGTAGAGTGTGGTGGCCCGCATCTCGGCGCATCTGTGTGGCGCGACGGGG 1422
 DB 2817 ATCCTCTCGTACAGTGGCTTCCACGCTCCACTCTTTATTCGCCGCTCCACCGGAGCG 2758
 OY 1423 CAGGGACGAGCGCGAGACAGGAACTGGCGGAGCGAAG-----GAGGGCGTTAGCG 1476
 DB 2757 CAGGGACCAACCCGATCACAGCGAATCTGTTCCAGCGCATTTCTTCCAGCGGTTAGCG 2698
 OY 1477 AAGGACATCCCGGGACGACGCGCGAGTGGGTTGGAGTCGATCGCTGTGGAGCGGCG 1536
 DB 2697 AACGCCATTCCTGGACCTACTTCCACACACTTACCTGTGTCAATGTCAAGTGTAGTGGC 2638
 OY 1537 TCGTGGCCCTCTCCATCGAGCTCGGGGAGAGCGGAGGATGAGGAGGTTGGGGCG 1596
 DB 2637 TCGTGTGCTTCTTCCACCGGAGATCTGCGGACGAGGATCGATGATGATGATGATGATG 2578
 OY 1597 CACTCCGGGGGAACCATGCGCGTCCCA 1522
 DB 2577 CATTCCGGTGAAGGATTTATCCCA 2552

RESULT 11
 AAC41895/c
 ID AAC41895 standard; DNA; 1024 BP.
 XX

AC AAC41895;
 XX 17-OCT-2000 (first entry)
 XX Arabidopsis thaliana DNA fragment SEQ ID NO: 33532.
 XX
 XX Hybridisation assay; genetic mapping; gene expression control;
 KW protein identification; signal transduction pathway;
 KW metabolic pathway; promoter; termination sequence; ss.
 XX
 OS Arabidopsis thaliana.
 XX
 XX EP1033405-A2.
 XX
 XX 06-SEP-2000.
 XX
 XX 25-FEB-2000; 2000EP-0301439.
 XX
 XX 25-FEB-1999; 99US-0121825.
 PR 05-MAR-1999; 99US-0123180.
 PR 09-MAR-1999; 99US-0123548.
 PR 23-MAR-1999; 99US-0125788.
 PR 25-MAR-1999; 99US-0126584.
 PR 29-MAR-1999; 99US-0126785.
 PR 01-APR-1999; 99US-0127462.
 PR 06-APR-1999; 99US-0128234.
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PR 18-JUN-1999; 99US-0139463.
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 PR 28-JUL-1999; 99US-0145951.
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 PR 03-AUG-1999; 99US-0147038.
 PR 04-AUG-1999; 99US-0147204.
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 PR 06-AUG-1999; 99US-0147303.
 PR 06-AUG-1999; 99US-0147416.
 PR 09-AUG-1999; 99US-0147493.
 PR 09-AUG-1999; 99US-0147935.
 PR 10-AUG-1999; 99US-0148171.
 PR 11-AUG-1999; 99US-0148319.
 PR 12-AUG-1999; 99US-0148341.
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 PR 17-AUG-1999; 99US-0149175.
 PR 18-AUG-1999; 99US-0149246.
 PR 20-AUG-1999; 99US-0149722.
 PR 20-AUG-1999; 99US-0149723.
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 PR 23-AUG-1999; 99US-0149902.
 PR 23-AUG-1999; 99US-0149930.
 PR 23-AUG-1999; 99US-0150566.

QY	1423	CAGGGGACGAGGCCGATGACAGGAA-----CTGGCCGAGGCGAAGAGGCGCTTACGG	1476
Db	468	CAGCGACCAACCCGATCAGACGCGAATCTGTTCCACGGCGATTCTTCAACGCGCTTACGG	409
QY	1477	AAGGACATCCCGGGACCGACGCGCAGGTGCGGTGGAGTGCATGCCGTTGTGGAGCGGC	1536
Db	408	AACGCAATCTCGGACCTACTCCACACACTTTACCTGTGTCAATGTCAACGTGTAGTGGC	349
QY	1537	TCGTGGGCGCTCCCTCCATCCGAGCTGCGGGAGAGCGGAGGATGGAGGGGTTGGGGCG	1596
Db	348	TCGTGTGCTTCTTCCACCGGAGATCTGGGACAGCGGAGATCGATGAGTTGGTGGC	289
QY	1597	CACTCGCGGGGACCATGCGCTCCAG	1623
Db	288	ATCCCGTGGGAGGATTTATCCCG	262
RESULT 12			
AAA79573/c			
ID	AAA79573 standard; cDNA; 547 BP.		
AC	AAA79573;		
XX	27-NOV-2000 (first entry)		
DE	Pinus radiata cell signalling involved polynucleotide SEQ ID NO:374.		
KW	Eucalyptus grandis; Pinus radiata; Monterey pine; plant; modification;		
KW	plant cell signalling; modulation; transgenic plant; pathogen; growth;		
KW	environmental change; development; cell proliferation; differentiation;		
KW	elongation; survival; disease resistance; nutrient metabolism; ss.		
OS	Pinus radiata.		
PN	WO20042171-A1.		
PD	20-JUL-2000.		
PF	11-JAN-2000; 2000WO-US00724.		
PR	12-JAN-1999; 99US-0228986.		
PR	01-NOV-1999; 99US-0162866.		
PA	(GENE-) GENESIS RES & DEV CORP LTD.		
PI	Strabala TJ, Nieuwenhuizen NJ;		
PI	WPI; 2000-476052/41.		
DR	Isolated polynucleotide encoding a polypeptide involved in cell		
PT	signaling used for generating transgenic plants with modified responses		
PT	to external signals -		
PS	Claim 1; Page 176; 527pp; English.		
CC	AAA79263 to AAA79736 and AAB35100 to AAB25570 represent polynucleotide		
CC	and protein sequences isolated from eucalyptus (Eucalyptus grandis) or		
CC	pine (Pinus radiata also known as Monterey pine). The protein sequences		
CC	are involved in cell signalling. The polynucleotide and protein		
CC	sequences can be used to modify the response of plant cells to external		
CC	signals e.g. environmental changes or pathogens during the growth and		
CC	development of a plant. They can be used to modify cell proliferation,		
CC	differentiation, elongation and survival, resistance to disease and		
CC	nutrient metabolism. Examples of modifications which can be produced are		
CC	altered fruit ripening and senescence of leaves and flowers e.g. to		
CC	delay senescence and prolong the life of cut flowers or enhance		
CC	senescence of reproductive organs to engineer sterile plants. Other		
CC	modifications can be used to delay senescence in selected cell types or		
CC	organs providing fruit and vegetables which have a longer shelf life		
CC	between harvest and consumption, or to decrease branching frequency in		
CC	forest tree species giving long stretches of valuable knot-free clear		
CC	wood which can be used in solid timber furniture and veneers.		

PT New isolated hypoxia inducible promoter

XX

PT New isolated hypoxia inducible promoter

Sequence 5526 BP; 1438 A; 1322 C; 1289 G; 1477 T; 0 other;

Sequence 15686 BP: 4645 A; 3184 C; 3204 G; 4653 T; 0 other;

QY	4181	CAACGTTTGACCAATTCGCTCTATTGTAAGAAAAGATATAGTAGTATGTTTATTCGTATT	4240
Db	9054	CCAACTTTGATCGCCGCTTTATTTTGAGAAAATTTTATAATAGTATTTTGTGTGTTATG	9113
QY	4241	AGATGATAAACAATGATAGTACTTTATGTCGTACTAAATTTTTTTTTTAATATTTTTTATT	4300
Db	9114	AGATGATAAATAATAATAGTACTTTACTCATGACT--TATGTTTTTAATTTTTTTTCAAA	9171
QY	4301	AAATTTTCAAATAAGACGGATGTCCTCAAAAGCGCTAAACATGATATCTATGGCGTCACTTA	4360
Db	9172	AAATTTTCAAATAGACAGACGATTAA--CTTGGCGCGCGGAAAACTATGTTTACACTTA	9229

05 4361 TTTTGGACGGAGGTAGTA 4379

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Search completed: March 26, 2003, 05:16:56

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GenCore version 5.1.4.p5.4578
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OM nucleic - nucleic search, using sw model

Run on: March 25, 2003, 13:50:00 ; Search time 5095.83 Seconds
(without alignments)
15894.084 Million cell updates/sec

Title: US-09-702-134-7212_COPY_62300_67300

Perfect score: 5001

Sequence: 1 aggggacactacattcca.....tgccgcggagtcgccccg 5001

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estlin:*
4: em_estmuv:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_estli:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_tod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
C 1	375.8	7.5	465	9	AU065751	AU065751	
C 2	334.4	6.7	498	9	AU030601	AU030601	
C 3	274.2	5.5	555	10	BE490225	BE490225 WHE0366_H	
C 4	254.6	5.1	309	14	D47552	D47552 RICS13122A	
C 5	230.4	4.6	381	14	BQ240809	BQ240809 TaE05012F	
C 6	210.6	4.2	486	17	AZ918792	AZ918792 1006008A0	

C 7	133	3.9	588	12	BF619879	BF619879 HVSMEC000
C 8	188.4	3.8	774	17	AQ576807	AQ576807 nbxb0089H
C 9	187.4	3.7	273	9	AU097543	AU097543 HVSME000
C 10	180	3.6	816	13	BI956651	BI956651 HVSME000
C 11	178.6	3.6	394	17	BH643146	BH643146 100805280
C 12	178.2	3.6	613	10	BE443619	BE443619 WHE1116_B
C 13	167	3.3	446	14	BQ237748	BQ237748 TaE05012F
C 14	164.8	3.3	535	17	AQ573895	AQ573895 nbxb0083A
C 15	163.6	3.3	842	17	AQ327645	AQ327645 nbxb0041B
C 16	162	3.2	589	17	AQ289925	AQ289925 nbxb0036E
C 17	161.6	3.2	689	17	AQ289077	AQ289077 nbxb0034K
C 18	161.4	3.2	502	12	BG560351	BG560351 RH122_73_
C 19	160.4	3.2	815	10	BE213308	BE213308 EST0065 T
C 20	160	3.2	579	17	AQ274081	AQ274081 nbxb0032M
C 21	157	3.1	757	17	AQ915616	AQ915616 nbxb0059C
C 22	153.2	3.1	600	17	AQ364616	AQ364616 nbxb0061G
C 23	153	3.1	423	12	BG102400	BG102400 RH122_23_
C 24	153	3.1	696	17	AQ689068	AQ689068 nbxb0078J
C 25	152.8	3.1	363	12	BF473797	BF473797 WHE0837_E
C 26	152.4	3.0	756	17	AQ689102	AQ689102 nbxb0033P
C 27	152.4	3.0	812	17	AZ135604	AZ135604 OSJNB0011
C 28	152.2	3.0	469	17	AQ446510	AQ446510 nbxb0070K
C 29	152.2	3.0	783	17	AQ863548	AQ863548 nbxb0021C
C 30	150.8	3.0	697	17	AQ579470	AQ579470 nbxb0084C
C 31	150.8	3.0	808	17	AQ794105	AQ794105 nbxb0052E
C 32	150.2	3.0	334	9	AL829579	AL829579 AL829579
C 33	146	2.9	610	17	AQ156838	AQ156838 nbxb0008D
C 34	145.8	2.9	665	17	AZ047724	AZ047724 nbxb0094A
C 35	144.4	2.9	720	17	AQ689393	AQ689393 nbxb0079B
C 36	144	2.9	583	14	BQ253395	BQ253395 san69f02_
C 37	141.8	2.8	667	17	AQ864314	AQ864314 nbxb0022N
C 38	141.8	2.8	763	17	AQ914146	AQ914146 nbxb0047M
C 39	140.8	2.8	735	17	AQ864484	AQ864484 nbxb0023I
C 40	140.8	2.8	847	17	AQ868460	AQ868460 nbxb0027J
C 41	139.8	2.8	657	17	AZ131579	AZ131579 OSJNB0011
C 42	139.6	2.8	554	13	B1129518	B1129518 G091P77Y
C 43	138.8	2.8	764	17	AQ914191	AQ914191 nbxb0047H
C 44	138.2	2.8	456	13	BF643717	BF643717 IPL 56_80
C 45	136	2.8	578	17	AQ509458	AQ509458 nbxb0096I

ALIGNMENTS

RESULT 1	AU065751/c	465 bp	mRNA	linear	EST 02-APR-2002
LOCUS	AU065751	Rice cDNA from immature leaf including apical meristem			
DEFINITION	Oryza sativa (japonica cultivar-group) cDNA clone B51292_1A, mRNA sequence.				
ACCESSION	AU065751				
VERSION	AU065751.1	GI:4968847			
KEYWORDS	EST.				
SOURCE	Oryza sativa (japonica cultivar-group).				
ORGANISM	Oryza sativa (japonica cultivar-group).				
REFERENCE	1 (bases 1 to 465)				
AUTHORS	Sasaki,T. and Yamamoto,K.				
TITLE	Rice cDNA from immature leaf including apical meristem				
JOURNAL	Unpublished (1997)				
COMMENT	Contact: takuji Sasaki National Institute of Agrobiological Resources Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan Tel: 81-298-38-7441 Fax: 81-298-38-7468 Email: tsasaki@affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/ PROJECT = "RGP" Location/Qualifiers 1. .465 /organism="Oryza sativa (japonica cultivar-group)"				

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/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="E51292_1A"
/clone_lib="Rice cDNA from immature leaf including apical meristem"
/dev_stage="immature"
/notes="Organ: leaf; immature leaf including apical meristem (under long day condition)"
meristem
BASE COUNT 72 a 160 c 138 g 90 t 5 others
ORIGIN

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Query Match 7.5%; Score 375.8; DB 9; Length 465;
Best Local Similarity 98.5%; Pred. No. 1e-57;
Matches 388; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 1426 GGCAGGAGCCGATGACAGGAAGTGGCCGGAGCGAGGAGGGGCTAGCGAAGGACATC 1485
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 393 GGGACCAAGCCGATWACAGGNAAGTGGCCGGAGCGAGGA-GGCGTTAGCGAAGGACATC 335
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1486 CCGGGACCGACCGCCAGGTGGGTTGGAGTCGATGCCGTTGTGGAGCGCTCGTGGGCC 1545
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 334 CCGGGACCGACCGCGAGGTGGGTTGGAGTCGATGCCGTTGTGGAGCGCTCGTGGGCC 275
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1546 TCCTCCATCGAGTCGCGGGAGAGCGGAGGATGGAGGGGTTGGGGGCGCACTCCGGG 1605
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 274 TCCTCCATCGAGTCGCGGGAGAGCGGAGGATGGAGGGGTTGGGGGCGCACTCCGGG 215
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1606 GGAACCATCGCTCCAGTGGACCCACACGCGCCCGCCGCGCCGCTGTTCCGACTGC 1665
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 214 GGAACCATCGCTCCAGTGGACCCACACGCGCCCGCCGCGCCGCTGTTCCGACTGC 155
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1666 CTCCGAGGATGAACACCACTGTTTCGACGGAGGGAGGACAGCGCGCGCGCGCCG 1725
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 154 CTCCGAGGATGAACACCACTGTTTCGACGGAGGGAGGACAGCGCGCGCGCGCGCCG 95
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1726 GGAAGCAGCAGCAACAGCAGCATCCGCGCATTCGCTGCTTCTACGCTTGGGCTGG 1785
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 94 GGAAGCAGCAGCAACAGCAGCATCCGCGCATTCGCTGCTTCTACGCTTGGGCTGG 35
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1786 GGCTGGGGGTTGGGTTTGGGCAATAATTG 1819
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 34 GGCTGGGGGTTGGGTTTGGGCAATAATTG 1
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RESULT 2
AU030601/c 498 bp mRNA linear EST 01-APR-2002
LOCUS
DEFINITION
AU030601 Rice cDNA from immature leaf including apical meristem
Oryza sativa (japonica cultivar-group) cDNA clone E51292_2Z, mRNA
sequence.
ACCESSION
AU030601
VERSION
AU030601.1 GI:3763862
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group).
ORGANISM
Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Eriartoideae; Oryzaceae; Oryza.
1 (bases 1 to 498)
Sasaki, T. and Yamamoto, K.
Rice cDNA from immature leaf including apical meristem
Unpublished (1997)
Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
305-8602, Japan
Tel: 81-298-38-7441
Fax: 81-298-38-7468
Email: tsasaki@nri.affrc.go.jp, URL: http://rgp.dna.affrc.go.jp/
PROJECT = "RGP".
POLYA=No.
FEATURES
Location/Qualifiers
source
1..498

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/organism="Oryza sativa (japonica cultivar-group)"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="E51292_2Z"
/clone_lib="Rice cDNA from immature leaf including apical meristem"
/dev_stage="immature"
/notes="Organ: leaf; immature leaf including apical meristem (under long day condition)"
meristem
BASE COUNT 128 a 125 c 118 g 127 t
ORIGIN

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Query Match 6.7%; Score 334.4; DB 9; Length 498;
Best Local Similarity 96.9%; Pred. No. 2.9e-50;
Matches 341; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 98 TTTTAATTATACCAAGCCCAATCAATATCAAGAATGAGTGGTCCATGAACTAAATAA 157
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 487 TTTTATATACCAAGCCCAATCAATATCAAGAATGAGTGGTCCATGAACTAAATAA 428
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 158 GAAAGTAGACATAGAGTGGTGGTCTCTTAGCTATTATCTGATATAAAGAAACACAC 217
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 427 GAAAGTAGACATAGAGTGGTGGTCTCTTAGCTATTATCTGATATAAAGAAACACAC 368
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 218 ACAGAGAGGACTAGAGGTGGAGTACCATAGTTCAAAATAGGCTTGAGCCACATATGTC 277
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 367 ACAGAGAGGACTAGAGGTGGAGTACCATAGTTCAAAATAGGCTTGAGCCACATATGTC 308
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 278 CAAGCTGACACTGGCTGGTGGTCTAAGTGCAGATGCCCATCTCTAGTGGCAACCTT 337
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 307 CAAGCTGACACTGGCTGGTGGTCTAAGTGCAGATGCCCATCTCTAGTGGCAACCTT 248
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 338 TTGCATCAACAAATCTCACGTTTCGAAAGTTTGATCCCTTCTGAGCTTCCCTTACTACTT 397
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 247 TTGCATCAACAAATCTCACGTTTCGAAAGTTTGATCCCTTCTGAGCTTCCCTTACTACTT 188
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 398 CAGTATATTGCCCAAGCCCTGATGCTAGTCCCTGAGTAAACCAACACAGAG 449
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 187 CAGTATATTGCCCAAGCCCTGATGCTAGTCCCTGAGTAAACCAACAGAGAGTG 136
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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RESULT 3
BE490225/c 555 bp mRNA linear EST 31-JUL-2000
LOCUS
DEFINITION
WHE0366_H01_P02Zs Wheat cold-stressed seedling cDNA library
Triticum aestivum cDNA clone WHE0366_H01_P02, mRNA sequence.
ACCESSION
BE490225
VERSION
BE490225.1 GI:9609758
KEYWORDS
EST.
SOURCE
Bread wheat.
ORGANISM
Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Triticum.
1 (bases 1 to 555)
Anderson, O.D., Choi, S., Choi, D.W., Close, T.J., Penton, R.D., Han
, P.S., Hsiao, C.C., Kang, Y., Lazo, G.R., Miller, R., Rausch, C.J.,
Seaton, C.L. and Tong, J.C.
The structure and function of the expressed portion of the wheat
genomes - Cold-stressed seedling cDNA library
Unpublished (2000)
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
Email: oanderson@w.usda.gov
Sequence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: Stratagene SK primer.
FEATURES
Location/Qualifiers
source
1..555

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REFERENCE	Ehrhartoideae; Oryzeae; Oryza.
AUTHORS	1 (bases 1 to 309)
TITLE	Sasaki, T., Miyao, A. and Yamamoto, K.
COMMENT	Rice CDNA from callus 1995 Unpublished (1995) Contact: Takuji Sasaki National Institute of Agrobiological Resources Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan Tel: 81-298-38-7441 Fax: 81-298-38-7468 Email: tsasaki@abr.affrc.go.jp, URL: http://rgp.dna.affrc.go.jp/ PROJECT: "RGP".
FEATURES	Location/Qualifiers
source	1..309 /organism="Oryza sativa (japonica cultivar-group)" /cultivar="Nipponbare" /db_xref="taxon:39947" /clone_lib="Rice green shoot" /note="Green shoot (8 days old)"
BASE COUNT	57 a 94 c 91 g 60 t
ORIGIN	7 others

Query Match	5.1%;	Score	254.6;	DB	14;	Length	309;
Best Local Similarity	93.9%;	Pred.	No. 8e-36;				
Matches	293;	Conservative	0;	Mismatches	16;	Indels	3;
						Gaps	
QY	4682	CCTGTCGCTCCACCTTCGTGCTTAATGCGTTCTAGCGTAGCGTAGCAGATCCACAA	4741				
Db	1	CCTGTCGCTCCACCTTCGTGCTTAATGCGTTCTAGCGTAGCGTAGCAGATCCACAA	59				
QY	4742	ACACCTAGCAGCAGCAGCATTTGGTAGCTACTCTCTAGTCTCTAGCTAGTAGTGAGCGT	4801				
Db	60	ACACCTAGCAGCAGCAGCATTTGGTAGCTACTCTCTAGTCTCTAGTAGTGAGTGAGCGT	119				
QY	4802	GAGGAGCAGTAGCAGCATGGCGTGGCGACAGTAAACGTGCAGGTACTAGCGTCTGCTCTGC	4861				
Db	120	GAGGAGCAGTAGCAGCATGGCGTGGCGACAGTAAACGTGCAGGTACTAGCGTCTGCTCTGC	178				
QY	4862	TGCTGCGCACACCGCCACGGCGCAGCGCGACGCGACGCGTGTATATCCTTTTGG	4921				
Db	179	TGCTGCTCACACCGNCCACGGCGCAGCGCGACGCGTGTATATCCTTTTGG	238				
QY	4922	GGGGGCGATCCACATATGGCGGTGCGGCGCGCGCCACCAACGGGCGGTGGAGCGGCGTGG	4981				
Db	239	GGGGGCGATCCACATATGGCGGTGCGGCGCGCGCCACCAACGGGCGGTGGAGCGGCGTGG	297				
QY	4982	TGCCGCGCGGAGT	4993				
Db	298	TGCCGCGCGGAGT	309				

RESULT 5
BQ240809/c
LOCUS
DEFINITION
BQ240809
TAE05012F06R TAE05 Triticum aestivum cDNA clone TAE05012F06S, mRNA
sequence.
ACCESSION
BQ240809
VERSION
BQ240809.1
KEYWORDS
GI:20436685
EST.
SOURCE
Bread wheat.
ORGANISM
Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
; Triticeae; Triticum.
1 (bases 1 to 381)
Cloutier,S
REFERENCE
Wheat functional genomics - Glenlea developing seeds cDNA libraries
Unpublished (2002)
AUTHORS
Contact: Dr. Sylvie Cloutier
JOURNAL
Cereal Research Centre, Agriculture and Agri-food Canada
COMMENT
195 Dafoe Rd, Winnipeg, MB, Canada R3T 2M9
Tel: (204) 983-2340

Sequence was trimmed at very probable ligation site. Post-ligation sequence submitted separately.

Plate: 1006008 row: 3

FEATURES	Location/Qualifiers
source	1 486

/cultivar="mixed background W23/A188/B73"

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/clone_lib="I006 - RescuemU Grld G"  
/tissue_type="leaf"
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./lab_host="DH10B"
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pBluescript backbone); Site_1: BamHI; Site_2: BglII;
RescueMu is a 4.9 kb modified maize Mu transposon

Mu elements insert preferentially into transcription

site www.zmdb.iastate.edu, and follow the links for 'RescueMu', Grid G was grown at Stanford in 2000. DNA was

and BglII, and ligated to form circular plasmids. DH10B

BASE COUNT	57 a	176 c	181 a	72 f
ampicillin,				

Best Local Similarity	74.28	Pred. NO. 6.3e-28;	
Matches	206	Conservative	0
Mismatches	0	Mismatches	94
		Indels	9
		Gaps	2

QY 1315 GCGCCGATGCGGCCGCCGGTCTCGAGGGCGACCTGGAGCGCGGACGAGATCGGAGTAG 1374

Db 483 GCACCGATGCGGGCCCCCGTCTCGACGGGACCCCTGGCCCCGGCGCAGCATCTCGGCGTAG 424

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Db 363 CCTACCAAGGCGCCCCCGCGGCGCGAGCGCAGCAGCGGTTGGCGAACGCCATCCCG 304

QY 1489 GGACCGACGCCGAGGTGCGGTT--GGAGTCGATGCCCGTTGTGGAGCGGCTCGTGGGCC 1545

Table 1

Variable	Mean	Standard Deviation	Minimum	Maximum
Age	34.5	12.5	18	65
Gender	0.5	0.5	0	1
Marital Status	0.3	0.5	0	1
Education	12.5	2.5	9	16
Income	3500	1500	1000	8000
Health	0.8	0.2	0	1
Smoking	0.2	0.4	0	1
Alcohol	0.1	0.3	0	1
Exercise	0.4	0.5	0	1
Stress	0.6	0.5	0	1
Sleep	0.7	0.4	0	1
Diet	0.5	0.5	0	1
Work	0.8	0.2	0	1
Family	0.6	0.5	0	1
Friends	0.7	0.4	0	1
Hobbies	0.5	0.5	0	1
Travel	0.3	0.5	0	1
Volunteering	0.2	0.4	0	1
Religion	0.4	0.5	0	1
Politics	0.5	0.5	0	1
Art	0.3	0.5	0	1
Music	0.4	0.5	0	1
Gardening	0.2	0.4	0	1
Fishing	0.1	0.3	0	1
Reading	0.6	0.5	0	1
Writing	0.2	0.4	0	1
Cooking	0.4	0.5	0	1
Cleaning	0.3	0.5	0	1
Shopping	0.5	0.5	0	1
Driving	0.7	0.4	0	1
Traveling	0.4	0.5	0	1
Volunteering	0.2	0.4	0	1
Religion	0.4	0.5	0	1
Politics	0.5	0.5	0	1
Art	0.3	0.5	0	1
Music	0.4	0.5	0	1
Gardening	0.2	0.4	0	1
Fishing	0.1	0.3	0	1
Reading	0.6	0.5	0	1
Writing	0.2	0.4	0	1
Cooking	0.4	0.5	0	1
Cleaning	0.3	0.5	0	1
Shopping	0.5	0.5	0	1
Driving	0.7	0.4	0	1
Traveling	0.4	0.5	0	1
Volunteering	0.2	0.4	0	1
Religion	0.4	0.5	0	1
Politics	0.5	0.5	0	1
Art	0.3	0.5	0	1
Music	0.4	0.5	0	1
Gardening	0.2	0.4	0	1
Fishing	0.1	0.3	0	1
Reading	0.6	0.5	0	1
Writing	0.2	0.4	0	1
Cooking	0.4	0.5	0	1
Cleaning	0.3	0.5	0	1
Shopping	0.5	0.5	0	1
Driving	0.7	0.4	0	1
Traveling	0.4	0.5	0	1
Volunteering	0.2	0.4	0	1
Religion	0.4	0.5	0	1
Politics	0.5	0.5	0	1
Art	0.3	0.5	0	1
Music	0.4	0.5	0	1
Gardening	0.2	0.4	0	1
Fishing	0.1	0.3	0	1
Reading	0.6	0.5	0	1
Writing	0.2	0.4	0	1
Cooking	0.4	0.5	0	1
Cleaning	0.3	0.5	0	1
Shopping	0.5	0.5	0	1
Driving	0.7	0.4	0	1
Traveling	0.4	0.5	0	1
Volunteering	0.2	0.4	0	1
Religion	0.4	0.5	0	1
Politics	0.5	0.5	0	1
Art	0.3	0.5	0	1
Music	0.4	0.5	0	1
Gardening	0.2	0.4	0	1
Fishing	0.1	0.3	0	1
Reading	0.6	0.5	0	1
Writing	0.2	0.4	0	1
Cooking	0.4	0.5	0	1
Cleaning	0.3	0.5	0	1
Shopping	0.5	0.5	0	1
Driving	0.7	0.4	0	1
Traveling	0.4	0.5	0	

QV 1606 GGAAACCATGCCGTCCACAGTGGGACCCCAACACGCCGCCGCCGCGCATGTTCGACTGC 1665

D_b 183 GGCACCAAAGTCCACAGCGGTTCGCCACCAACCCGCGCGCGCATGTTGGACTGC 124

QY 1666 CCITCCAGGATGAACACCACTTGTTCGACGGAGGAGG 1704

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RESULT 7
DEC 1 00 30 15

LOCUS	BF019873	508 bp	RNA	EST	EST 22 Oct 2001
DEFINITION	HVSMC0009122f	Hordeum vulgare seedling shoot	EST library		

QY	1243	GCATCCGGCGGGCGTACTGTTGGCGTCGGCCACGACGACGGTGTGCTCTCCCCCTGG	1302
Db <th>515</th> <th>TCCAGCTTCCCTTGGTATTCGGCGCGCTTTCGGCATCGGCATATGATCATCGCTCTCCCCCTGG</th> <th>456</th>	515	TCCAGCTTCCCTTGGTATTCGGCGCGCTTTCGGCATCGGCATATGATCATCGCTCTCCCCCTGG	456
QY <th>1303</th> <th>TACCAGAGGACACGCGCATGCGCGCGCGCTCTCGAGGGCGACCCCTGGAGCGCGCGAAG</th> <th>1362</th>	1303	TACCAGAGGACACGCGCATGCGCGCGCGCTCTCGAGGGCGACCCCTGGAGCGCGCGAAG	1362
Db <th>455</th> <th>TACCACAGACAGCGCTCGAT--CTCTCCGCACTCGGTCGCGCGCGCGCGCGCGAC</th> <th>399</th>	455	TACCACAGACAGCGCTCGAT--CTCTCCGCACTCGGTCGCGCGCGCGCGCGCGAC	399
QY <th>1363</th> <th>AGATCGGAGTAGAGTTCGGTTCGGTTCGGCCAGTTCGGCCATCTCTGGTTCGGCGCGAGCGGG</th> <th>1422</th>	1363	AGATCGGAGTAGAGTTCGGTTCGGTTCGGCCAGTTCGGCCATCTCTGGTTCGGCGCGAGCGGG	1422
Db <th>398</th> <th>ATCTGCTCGTACAGGTGCTTCGCCCGCGGGCCCACTCCCGGATGCGCGCTCGCGCAACGGCG</th> <th>339</th>	398	ATCTGCTCGTACAGGTGCTTCGCCCGCGGGCCCACTCCCGGATGCGCGCTCGCGCAACGGCG	339
QY <th>1423</th> <th>CAGGGGACGAG-----GCCGATGACAGGGAACCTGCGCGAGCGAAGAGGGCGTTTA</th> <th>1473</th>	1423	CAGGGGACGAG-----GCCGATGACAGGGAACCTGCGCGAGCGAAGAGGGCGTTTA	1473
Db <th>338</th> <th>CACGGTACGAGCCCTTACCCCGCGGTCCTTGGGGCTGACGTCGCGGAGATGCGCGCG</th> <th>279</th>	338	CACGGTACGAGCCCTTACCCCGCGGTCCTTGGGGCTGACGTCGCGGAGATGCGCGCG	279
QY <th>1474</th> <th>CGAAGGACATCCCGGGACCGACCGCAGCTCGGTTGGAGTCGATCCGTTTGTGAGC</th> <th>1533</th>	1474	CGAAGGACATCCCGGGACCGACCGCAGCTCGGTTGGAGTCGATCCGTTTGTGAGC	1533
Db <th>278</th> <th>CGAAGGCCATCCCGGGCGGACCGCAGGCTCTTGGTCGTGATGTCGGCGTGCAGC</th> <th>219</th>	278	CGAAGGCCATCCCGGGCGGACCGCAGGCTCTTGGTCGTGATGTCGGCGTGCAGC	219
QY <th>1534</th> <th>GGCTGCTGGCTCTCCCATCGAGCTGCGGGGACGAGCGGAGATGAGGGGTTGGGG</th> <th>1593</th>	1534	GGCTGCTGGCTCTCCCATCGAGCTGCGGGGACGAGCGGAGATGAGGGGTTGGGG	1593
Db <th>218</th> <th>GGCTGCTGGGCTCTCCCATCGAGCGAGCGGAGAGCGGAGATGAGGGGTCGGCG</th> <th>159</th>	218	GGCTGCTGGGCTCTCCCATCGAGCGAGCGGAGAGCGGAGATGAGGGGTCGGCG	159
QY <th>1594</th> <th>GCGCACTCCGGGGGAACCATGCGCTCCCATGTTGGAGCCCAACACCGCCCGCGCCCGC</th> <th>1653</th>	1594	GCGCACTCCGGGGGAACCATGCGCTCCCATGTTGGAGCCCAACACCGCCCGCGCCCGC	1653
Db <th>158</th> <th>GCGCACTCCGGGGGACGACACCCATCCACCGCGCTGTCACGCGCGCGCGCGCGC</th> <th>99</th>	158	GCGCACTCCGGGGGACGACACCCATCCACCGCGCTGTCACGCGCGCGCGCGCGC	99
QY <th>1654</th> <th>ATGTTGACTGTCCTCCAGGATGACACCACTTGTTCGAGGAGGAGGACACAGC</th> <th>1713</th>	1654	ATGTTGACTGTCCTCCAGGATGACACCACTTGTTCGAGGAGGAGGACACAGC	1713
Db <th>98</th> <th>ATGTTGCTTCTGCTCCCTGACAGAGGAAGATGCGATGACTGCGGCGCTGCGGAGCAGCGC</th> <th>39</th>	98	ATGTTGCTTCTGCTCCCTGACAGAGGAAGATGCGATGACTGCGGCGCTGCGGAGCAGCGC	39
QY <th>1714</th> <th>G 1714</th> <th></th>	1714	G 1714	
Db <th>38</th> <th>G 38</th> <th></th>	38	G 38	
RESULT 8			
AQ576807/c			
LOCUS	AQ576807	774 bp	DNA linear GSS 02-JUN-1999
DEFINITION	nxbx0085H04r CUGI Rice BAC Library Oryza sativa genomic clone		
ACCESSION	nxbx0085H04r, DNA sequence.		
VERSION	AQ576807.1		
KEYWORDS	GSS.		
SOURCE	Oryza sativa.		
ORGANISM	Oryza sativa		
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;		
AUTHORS	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;		
TITLE	Ehrnartideae; Oryzeae; Oryza.		
JOURNAL	1 (bases 1 to 774)		
COMMENT	Wing/R.A. and Dean,R.A. A BAC End Sequencing Framework to Sequence the Rice Genome Unpublished (1998) Contact: Wing RA Clemson University Genomics Institute 100 Jordan Hall, Clemson, SC 29634, USA Tel: 864 656 7288 Fax: 864 656 4293 Email: rwing@clemson.edu Seq primer: GGAAACGCTATGACCATG Class: BAC ends High quality sequence stop: 465. Location/Qualifiers 1..774 /organism="Oryza sativa" /strain="Japonica" /cultivar="Nipponbare" /db_xref="taxon:4530" /clone="nxbx0085H04r" /clone_lib="CUGI Rice BAC Library" /tissue_type="leaf"		
FEATURES			
source			

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FEATURES
source
Location/Qualifiers
1. .273
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/dev_stages="Etiolated shoot (8 days old)"
/note="Etiolated shoot (8 days old)"
BASE COUNT      87 a      50 c      37 g      72 t      27 others
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Query Match      3.7%; Score 187.4; DB 9; Length 273;
Best Local Similarity 85.3%; Pred. No. 1.1e-23;
Matches 191; Conservative 0; Mismatches 33; Indels 0; Gaps 0;
QY 98 TTTAATTATACCAGCAATTCAAATAATCATAGATAGTGGTCATGAAACTAAATAA 157
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 224 TTTTTTTAAACCAAGCAATTCAAANAACNANGANGNGNCANGAACTAAATAA 165
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 158 GAARAGTAGACATAGGTCCTACTCTCTTAGCTATTTATCTGTATGAAGAAACCAAC 217
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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QY	218	ACAGAGGAGCTAGAGCGTGGAGTAGCATCATAGTTTCAATAGGCTTGAGCCAAACATATGTC	277
Db	104	ACAGNGNGGNCCTAGAGCGGGAAGTNCNCNTAGTTTCAAAAAGGNTTNGGCCAACANATGCC	45
QY	278	CAAGCTGGACTTCGGTTGGTGGCTAAAGTGCAGATGCCCATCT	321
Db	44	CAAGCTGGACTTCGGCTTGGTGGCTAAGTGCAGATGCCCATCT	1

RESULT 10
 LOCUS BI956651/c
 DEFINITION
 (normal) Hordeum vulgare cDNA clone HVSMEN0004J09f, mRNA sequence.
 VERSION BI956651
 KEYWORDS EST.
 SOURCE Hordeum vulgare.
 ORGANISM Hordeum vulgare
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticeae. Hordeum

AUTHORS Wing, R., Closer, I. J., Kiehlmoors, A., Wise, R., Chin, A., Begum, D.,
 Frisch, D., Atkins, M., Yu, Y., Henry, D., Palmer, M., Rambo, T., Simmonds,
 J., Oates, R. and Main, D.
 TITLE Development of a genetically and physically anchored EST resource
 for barley genomics: Morex rachis cDNA library
 JOURNAL Unpublished (2001)
 COMMENT Contact: Wing RA
 Clemson University
 Clemson University
 100 Jordan Hall, Clemson, SC 29634, USA
 Tel: 864 656 7288
 Fax: 864 656 4293
 Email: rwing@clemson.edu
 Total hg bases = 236
 Seq primer: AATTAACCTCCTACATAAGGG
 High quality sequence stop: 372.
 FEATURES Location/Qualifiers
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 /organism="Hordeum vulgare"
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 /clone_lib="Hordeum vulgare rachis EST library HVCDA0015"
 (normal)
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 /lab_host="FJ121"

ORGANISM *Triticum aestivum*
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
 ; Triticeae; Triticum.

REFERENCE 1 (bases 1 to 613)
 AUTHORS Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han
 ,P.S., Hsia,C.C., Kang,Y., Iazo,G.R., Miller,R., Nguyen,H.T.,
 Rausch,C.J., Seaton,C.L., Tong,J.C. and Zhang,D.
 TITLE The structure and function of the expressed portion of the wheat
 genomes - Normalized root cDNA library

JOURNAL Unpublished (2000)
 COMMENT Contact: Olin Anderson
 US Department of Agriculture, Agriculture Research Service, Pacific
 West Area, Western Regional Research Center
 800 Buchanan Street, Albany, CA 94710, USA
 Tel: 5105595773
 Fax: 5105595818
 Email: oanderson@pw.usda.gov
 Sequence have been trimmed to remove vector sequence and low
 quality sequence with phred score less than 20
 Seq primer: Stratagene SK primer.

FEATURES
 source Location/Qualifiers
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 /db_xref="taxon:4565"
 /clone="WHE1116_B08.D16"
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 /dev_stage="Five day old etiolated seedling"
 /lab_host="E. coli DH10B"
 /note="Vector: Lambda Uni-ZAP XR, excised phagemid
 pBlueScript SK; Site_1: EcoRI; Site_2: XhoI; Seeds were
 surface-sterilized, germinated and grown aseptically in
 the dark at room temperature on filter paper with water,
 nystatin and ceftotaxime in covered crystallization
 dishes. Roots were harvested. The tissue, total RNA, and
 poly(A) RNA were prepared, a cDNA library was made in the
 T7 Close lab (Choi, Close, Fenton) at the University of
 California, Riverside. The cDNA clones were in vivo
 excised to give pBlueScript phagemids before
 normalization was carried out. The mass excision of
 phagemid library and normalization were done in HT Nguyen
 lab by D. Zhang at Texas Tech University. Normalization
 protocol used was that of Soares. Plasmid DNA
 preparations and DNA sequencing were performed in the OD
 Anderson lab (all other authors)."
 BASE COUNT 144 a 165 c 159 g 145 t
 ORIGIN
 Query Match 3.6%; Score 178.2; DB 10; Length 613;
 Best Local Similarity 68.5%; Pred. No. 4.2e-22;
 Matches 280; Conservative 0; Mismatches 118; Indels 11; Gaps 2;
 QY 28 AAGTGTAAACACACTAATGGTCAATCCGCTACTCATTAATGATGAAGTTGCTAGTGGCTA 87
 DB 565 AACTGCAGGACTCCGGTGGTTCCTCATTCATTCATGATGAAGAACTTGTACTGAATTA 506
 QY 88 AATTGGAAAATTAATTATACCAAGCAATTCATTAATCAATGAAGTGGTGCATCA 147
 DB 505 CATTTGCATAT-----TTATACCAATCAATTCATGATTAAGAAATGGTGGCCAGG 450
 QY 148 AACTAAATAGAAAAGTAGACATAGGTCGCTAGTCTCTTAGCTATTTATCTGATAAAA 207
 DB 449 AAGAGTTTCAGAGAGGAATTAACCAAGTAGTAGAGGACCAATAAATAGTTTCCCTTTAGA 390
 QY 208 GAAAAACACACAGACAGACTAGAGCGTGGAAAGTACACATAGTTCAAATAGGCTTGAGCC 267
 DB 389 GCT-----ACCGGGAGAACTAGTGTGTAATGTACCAATAGTCAATAGGACTTGAGCC 337
 QY 268 AACATATGCCAAGCTGACTTGGCTTGGGTCTAAGTGCAGATGCCATCTTCTACT 327

Db 336 AGCATATGTCCAGCTGGACCTGAGCCTGGGTGTTAAGATCAGATGCCGCTGTTGGAAC 277
 QY 328 GGCARACCCCTTGATCAACAAATCTCAGCTTCGAGTTTGATCCCTTTCTGAGCTTCC 387
 Db 276 GGCARACCCCTTGATCAACAACTCAGCTTCGAGAGTTTAAAGCCCTTCTGAGCTTCC 217
 QY 388 CTTACTACTTTCAGTATATTCGCCAAGCCCTGATGCTAGTCTCCTACTGAA 436
 Db 216 CTTACGACTTCGGTGTACTGCCCAAGCCCTGATGCCAGCCCACTCGA 168

RESULT 13
 BQ237748 446 bp mRNA linear EST 03-MAY-2002
 LOCUS TaE05012F06F TaE05 Triticum aestivum cDNA clone TaE05012F06F, mRNA
 DEFINITION sequence.
 ACCESSION BQ237748.1 GI:20433624
 VERSION BQ237748.1
 KEYWORDS EST.
 SOURCE bread wheat.
 ORGANISM Triticum aestivum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
 ; Triticeae; Triticum.

REFERENCE 1 (bases 1 to 446)
 AUTHORS Cloutier,S.
 TITLE Wheat functional genomics - Glenlea developing seeds cDNA libraries
 JOURNAL Unpublished (2002)
 COMMENT Contact: Dr. Sylvie Cloutier
 Cereal Research Centre, Agriculture and Agri-food Canada
 195 Dafoe Rd, Winnipeg, MB, Canada R3T 2M9
 Tel: (204) 983-2340
 Fax: (204) 983-4604
 Email: scloutier@am.agr.ca
 was cloned directionally, not all sequences generated with reverse
 primer were from the 5' end (same with forward primer and 3' end).
 Average insert size is >2.0 kb
 Plate: 012 row: F column: 06
 Seq primer: M13 Forward.

FEATURES
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 /cultivar="Glenlea"
 /db_xref="taxon:4565"
 /clone="TaE05012F06F"
 /clone_lib="TaE05"
 /tissue_type="developing seeds"
 /dev_stage="5 days after anthesis"
 /lab_host="E. coli DH10B"
 /note="Vector: pSPORT-P (Invitrogen Technologies); Site_1:
 NotI; Site_2: MluI; mRNA obtained from wheat seeds of
 cultivar Glenlea 5 days post-anthesis"
 BASE COUNT 132 a 100 c 107 g 107 t
 ORIGIN
 Query Match 3.3%; Score 167; DB 14; Length 446;
 Best Local Similarity 66.7%; Pred. No. 4.7e-20;
 Matches 273; Conservative 0; Mismatches 125; Indels 11; Gaps 2;
 QY 28 AAGTGTAAACACACTAATGGTCAATCCGCTACTCATTAATGATGAAGTTGCTAGTGGCTA 87
 DB 5 AACTGCAGGACTCCGGTGGTTCCTCATTCATTCATGATGAAGAACTTGTACTGAATTA 64
 QY 88 AATTGGAAAATTAATTATACCAAGCAATTCATTAATCAATGAAGTGGTGCATCA 147
 Db 65 CATTTGCATAT-----TTATACCAATCAATTCATGAATTTTAAAAATGGGGTGGCAGCG 120
 QY 148 AACTAAATAGAAAAGTAGACATAGGTCGCTAGTCTCTTAGCTATTTATCTGATAAAA 207
 Db 121 AAGAGTTTCAAGAGGAAATTAACCCAGAGTAGTAGAGCAATAAATAATGGATCCCTTTAAA 180
 QY 208 GAAAAACACACAGAGGAGGACTAGAGCGTGGGTCTAAGTGCAGATGCCATCTTCTACT 267

Query Match 3.3%; Score 164.8; DB 17; Length 535;
Best Local Similarity 85.8%; Pred. No. 1.1e-19;
Matches 218; Conservative 0; Mismatches 32; Indels 4; Gaps 3;

QY 4126 TAGATAGTACTCCCTCCGCTCAAAATAAGTGTAGTGTTCAGCTATTCAATGTTCAACG 4185
DB 272 TATACTCTACTCCCTCTGTCCCAATAAGTGCAGTTT-GCACTATTCACTTCACG 214
QY 4186 TTTGACCATCGCTCTATTGTTGAAAAGATATGATAGTATTTTATGTTATAGTAG 4245
DB 213 TTGACCGCTCGCTCTATTGTTGAAAATTTTTTATGATAGTATTTTATGCTATTAATG 154
QY 4246 ATAAAAATCAATAGTAGTACCTTTATGTTGCTACATAATTTTTTAAATATTTTATTAATTT 4305
DB 153 ATATACATGATAGTACCTTTATGTTGCTACATA--ATAATTTCAATTTTTCACAAATTT 96
QY 4306 TTCAATAAGACGAGTGTGCAAGCGCTTAACATGGATATCTATGCTACACTTATTTTG 4365
DB 95 TTCAATAAGACGAGGCTCAAA-CGTTGGACGGATATCCATGCTGTACTTATTTTG 37
QY 4366 GGACGGAGGTAGTA 4379
DB 36 GGACGGAGGTAGTA 23

RESULT 15
AQ327645/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AQ327645
nxb0041B05f CUGI Rice BAC Library Oryza sativa genomic clone
nxb0041B05f, DNA sequence.
AQ327645.1 GI:4119495
GSS.
Oryza sativa.
Oryza sativa.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 842)
Wing, R.A. and Dean, R.A.
A BAC End Sequencing Framework to Sequence the Rice Genome
Unpublished (1998)
Contact: Wing RA
Clemson University
Clemson University Genomics Institute
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: TAATACGATCTCATATAGG
Class: BAC ends
High quality sequence start: 58
High quality sequence stop: 189.
Location/Qualifiers
1. 842
/organism="Oryza sativa"
/strain="Japonica"
/cultivar="Nipponbare"
/db_xref="taxon:4530"
/clone="nxb0041B05f"
/clone_lib="CUGI Rice BAC Library"
/tissue_type="Leaf"
/lab_host="E. coli DH10B"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
HindIII; Rice is one of two most popular grains in the
world. Half of the world population especially those
inhabiting highly populated areas of the humid tropics
and subtropics, rely on rice as their primary source of
carbohydrate. Monocotyledonous rice is a diploid plant
(2n=24) with a haploid genome equivalent of 431 Mbp
(Arumuganathan and Earle, 1991). The relatively small
genome of rice, three times larger than that of

FEATURES
source

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OM nucleic - nucleic search, using sw model

Run on: March 26, 2003, 04:38:30 ; Search time 123.698 Seconds
(without alignments)
12398.686 Million cell updates/sec

Title: US-09-702-134-7212_COPY_62300_67300
Perfect score: 5001
Sequence: 1 aggggacactacatttcca.....tgccgcggagtgccgcccg 5001

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PCUS_COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	91.6	1.8	1730	4	US-09-575-574-5
C 2	91.6	1.8	3572	4	US-09-575-574-3
C 3	75.6	1.5	500	4	US-09-575-574-2
C 4	74	1.5	1926	4	US-09-249-585A-4
C 5	74	1.5	1931	2	US-09-130-114-2
C 6	73.2	1.5	1026	4	US-09-105-390-13
C 7	73.2	1.5	2169	4	US-09-105-390-5
C 8	70.6	1.4	7218	1	US-08-332-463-14
C 9	61	1.2	4403765	4	US-09-103-840A-2
C 10	61	1.2	4411529	4	US-09-103-840A-1
C 11	60.6	1.2	1280	4	US-09-060-756-4
C 12	60.6	1.2	15872	4	US-09-105-537-1
C 13	60.4	1.2	1591	4	US-08-728-956-3
C 14	60	1.2	390	4	US-09-197-649-7
C 15	60	1.2	925	3	US-08-858-003-1
C 16	60	1.2	925	3	US-09-078-166-1
C 17	60	1.2	925	4	US-08-397-467-1
C 18	60	1.2	4403765	4	US-09-103-840A-2
C 19	57.6	1.2	1881	4	US-09-434-288-5
C 20	57.2	1.1	4411529	4	US-09-103-840A-1
C 21	56.2	1.1	1590	4	US-09-434-288-1
C 22	56	1.1	1998	6	5212296-8
C 23	54.8	1.1	1138	3	US-08-381-148C-3
C 24	54.8	1.1	1884	1	US-07-704-288C-1
C 25	54.8	1.1	1884	1	US-08-379-259-1
C 26	54.4	1.1	12588	2	US-08-387-942C-1
C 27	54.4	1.1	28958	1	US-08-258-261B-6

C 28	54.4	1.1	28958	1	US-08-456-837-6	Sequence 6, Appli
C 29	54.4	1.1	28958	1	US-08-457-342-6	Sequence 6, Appli
C 30	54.4	1.1	28958	1	US-08-457-646A-6	Sequence 6, Appli
C 31	54.4	1.1	28958	1	US-08-458-076A-6	Sequence 6, Appli
C 32	54.4	1.1	28958	1	US-08-764-233A-4	Sequence 6, Appli
C 33	54.4	1.1	28958	1	US-08-457-335A-6	Sequence 6, Appli
C 34	54.4	1.1	28958	1	US-08-729-214-6	Sequence 6, Appli
C 35	54.4	1.1	28958	3	US-09-028-934-6	Sequence 6, Appli
C 36	54.4	1.1	49377	1	US-08-764-233A-1	Sequence 1, Appli
C 37	54.2	1.1	38506	3	US-09-320-878-19	Sequence 19, Appli
C 38	54	1.1	6085	4	US-09-029-603-4	Sequence 14, Appli
C 39	54	1.1	7218	1	US-08-232-463-14	Sequence 14, Appli
C 40	53.8	1.1	1439	4	US-09-056-556-167	Sequence 167, App
C 41	53.8	1.1	1439	4	US-09-072-596-162	Sequence 162, App
C 42	53.6	1.1	2064	1	US-08-343-428-1	Sequence 1, Appli
C 43	53.6	1.1	44377	2	US-08-804-227C-7	Sequence 7, Appli
C 44	53.6	1.1	44377	2	US-08-804-198-1	Sequence 1, Appli
C 45	53.2	1.1	1140	3	US-09-023-173-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-09-575-574-5/C
; Sequence 5, Application US/09575574
; Patent No. 6376750
; GENERAL INFORMATION:
; APPLICANT: Yu, Su-May
; APPLICANT: Chao, Yu-Chan
; TITLE OF INVENTION: PLANT SEEDLING AND EMBRYO PROMOTER
; FILE REFERENCE: 08919-047001
; CURRENT APPLICATION NUMBER: US/09575,574
; CURRENT FILING DATE: 2000-05-22
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1730
; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-575-574-5

Query Match 1.8%; Score 91.6; DB 4; Length 1730;
Best Local Similarity 65.6%; Pred. No. 2.4e-12;
Matches 168; Conservative 0; Mismatches 79; Indels 9; Gaps 2;

QY	4171	TATTCATGTTCCACCTTTGACCATTCGCTCTATTTCGAAAAAGATTATGATTAGTATTTT	4230
DB	1352	TTTCGTCGTCACCGTTAACTGTCCTTATATGAAAAATTTTATAATTAGTATTTT	1293
QY	4231	TATGTTATTAGATGATAAAACATGACTTATGTTGCTGACTATTTTATTTTAAAT	4290
DB	1292	CAUTGTTGTTATATGATAAAATATGATTAACTTTATACGTAACCTGCCTTTT	1237
QY	4291	ATTTTATTATTTTTCAAATAGACGGATGTCGTAACCGCTAAACATGATATCTATG	4350
DB	1236	TTTTTCATAATTTTTCAAAATA-----TGATCAAAACATTTGGACATGAAACCTCAGG	1182
QY	4351	GCACACTTATTTTGGCGGAGGTAGTACGCTATAAACACAGCTATAAACATATAA	4410
DB	1181	GTTTGTCCTTTTGGGACGGAGGAGTAACTCGTAGTCAGCGGTAGCACTACT	1122
QY	4411	GAGATAAAAGAGAAGA 4426	
DB	1121	CAATTATCAATATA 1106	

RESULT 2
US-09-575-574-3/C
; Sequence 3, Application US/09575574
; Patent No. 6376750
; GENERAL INFORMATION:
; APPLICANT: Yu, Su-May

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; APPLICANT: Chao, Yu-Chan
; TITLE OF INVENTION: PLANT SEEDLING AND EMBRYO PROMOTER
; FILE REFERENCE: 08919-047001
; CURRENT APPLICATION NUMBER: US/09/575,574
; CURRENT FILING DATE: 2000-05-22
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 3572
; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-575-574-3

Query Match      1.8%; Score 91.6; DB 4; Length 3572;
Best Local Similarity 65.6%; Pred. No. 3.6e-12;
Matches 168; Conservative 0; Mismatches 79; Indels 9; Gaps 2;

QY 4171 TATTCATGTCACGTTTGACCATCGCTTATTTGAAAAAGATTATGATTAGTATTTT 4230
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DB 1352 TTTTCGTGCCAACGTTTAACTGTCGCTTATATGAAAAATTTTATATAGTATTTT 1293
      ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 4231 TATGTTTATAGATGAATAACATAGTAGTACTTTTATGTGACTAATTTTTTTTAAAT 4290
      ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1292 CATTTGTTATATGATAAATATGATAATTAATCTTTATACGTAACCTGGCTTTT---AA 1237
      ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 4291 ATTTTATTTTAAATTTTCAAAATAGCGGATGTCAAAAGCGCTAAACATGATATCTATG 4350
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DB 1236 TTTTTCATAAATTTTTCANAATAA-----TGATCAAACTATGCAATCAAACTCAGG 1182
      ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 4351 GCTACACTTATTTTGGGACGAGTAGTAGGTATTAACACAGCTATTAACATATTTTAAA 4410
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DB 1181 GTTTGCTCTTTTGGGACGAGGAGTAAACTCGTAGCTAGCTCAGACGCGTAGCATACT 1122
      ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 4411 GAGATAAAAGAGAGA 4426
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DB 1121 CAATTATCAATATA 1106
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RESULT 3
US-09-575-574-2/c
; Sequence 2, Application US/09575574
; Patent No. 6376750
; GENERAL INFORMATION:
; APPLICANT: Chao, Yu-Chan
; TITLE OF INVENTION: PLANT SEEDLING AND EMBRYO PROMOTER
; FILE REFERENCE: 08919-047001
; CURRENT APPLICATION NUMBER: US/09/575,574
; CURRENT FILING DATE: 2000-05-22
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 500
; TYPE: DNA
; ORGANISM: Oryza sativa
US-09-575-574-2

Query Match      1.5%; Score 75.6; DB 4; Length 500;
Best Local Similarity 76.2%; Pred. No. 8.7e-09;
Matches 93; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

QY 4171 TATTCATGTCACGTTTGACCATCGCTTATTTGAAAAAGATTATGATTAGTATTTT 4230
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DB 122 TTTTCGTGCCAACGTTTAACTGTCGCTTATATGAAAAATTTTATATAGTATTTT 63
      ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 4231 TATGTTTATAGATGAATAACATAGTAGTACTTTTATGTGACTAATTTTTTTTAAAT 4290
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DB 62 CATTTGTTATATGATAAATATGATAATTAATCTTTATACGTAACCTGGCTTTTAAATTT 3
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QY 4291 AT 4292
      |
DB 2 TT 1
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RESULT 4
US-09-249-585A-4/c
; Sequence 4, Application US/09249585A
; Patent No. 6417002
; GENERAL INFORMATION:
; APPLICANT: Horlick, Robert
; TITLE OF INVENTION: METHOD FOR MAINTENANCE AND SELECTION OF EPISOMES
; FILE REFERENCE: 0867/0D905
; CURRENT APPLICATION NUMBER: US/09/249,585A
; CURRENT FILING DATE: 1999-02-11
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 1926
; TYPE: DNA
; ORGANISM: Epstein Barr Virus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1926)
; OTHER INFORMATION: template strand of EBNA-1 DNA
US-09-249-585A-4

Query Match      1.5%; Score 74; DB 4; Length 1926;
Best Local Similarity 47.1%; Pred. No. 4.5e-08;
Matches 227; Conservative 0; Mismatches 255; Indels 0; Gaps 0;

QY 1145 GATPAGAGAAAAAGAGAGAAATATATTAAGGGATAATACCTGGATGAGGAGAGGTGTG 1204
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DB 980 GGTGGAGACGAGGACGGGAGGACGAGGACGGGAGGAGGACGAGGACGGGAGGAGCGG 921
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QY 1205 GCATGGCAGATCGCGCGCAGGTGCGGACGAGCATCGCCATCCGCGGGCGTACTCGT 1264
      ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 920 GGAGGACGAGGACGGGAGGACGGGAGGACGGGAGGACGGGAGGACGGGAGGACGAGGA 861
      ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1265 TGGCTGTCGCCCCACGCGCACGCTGTCTCTCCCTCTGTTACGAGGACAGCGCCGATGC 1324
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DB 860 CGGGAGAGACGGGGAGGAGGACGAGGACGGGAGGACGGGAGGAGGACGAGGACGGGGA 801
      ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1325 GGCGCGCGGTCTCGAGGCGGACCCCTGGAGCGCGCAGCATCGGATAGAGTACGCTGTC 1384
      ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 800 GGACGGGAGGACGAGGACGGGAGGACGGGAGGACGGGAGGACGGGAGGAGGAGGA 741
      ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1385 CCTTGGCCCCAGTCGCCCATCTCTGTGCGCGCAGCGCGGCGGACGAGCGCCGATGACAG 1444
      ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 740 CGAGGACGCGGGAGGACGAGGACGGGAGGACGAGGACGGGAGGACGAGGACGGGAGGA 681
      ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1445 GGAACCTGCGCGGAGCGAAGAGGCGCTTAGCGAAGGACATCCCGGGACCGACGCCGAGG 1504
      ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 680 CGGGGAGGACGGGGAGGAGGACGAGGACGGGAGGACGGGAGGACGGGAGGACGGGAGGA 621
      ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1505 TCGGTTGGAGTCGATGCCGTTGTGGAGCGGCTCGTGGGCGCTCTCCCTCCATCGGAGTGG 1564
      ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 620 CGGGGAGGACGAGGACGGGAGGAGGACGAGGACGGGAGGACGGGAGGACGGGAGGAGGA 561
      ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1565 GGGAGAGCGGAGGATGAGGGGTTGGGGCGCAGCTCCGGGGGAACCATCGCTGCCAT 1624
      ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 560 GGACGAGGACGGGGAGGACGCGGGAGGAGGACGAGGACGGGAGGAGGACGAGGACGGGGA 501
      ||||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1625 GG 1626
      ||
DB 500 GG 499
      ||

RESULT 5
US-09-130-114-2/c
; Sequence 2, Application US/09130114
; Patent No. 5976807
; GENERAL INFORMATION:
; APPLICANT: Horlick, Robert A.
; APPLICANT: Damaj, Bassam B.
; APPLICANT: Robbins, Alan K.
; TITLE OF INVENTION: Eukaryotic Cells Stably Expressing Genes
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RESULT 7
US-09-105-390-5
Sequence 5, Application US/09105390
Patent No. 6288303
GENERAL INFORMATION:
APPLICANT: Rodriguez, Raymond
TITLE OF INVENTION: Rice Beta-Glucanase Enzymes
TITLE OF INVENTION: and Genes
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Denlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fastseq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09105,390
FILING DATE: Filed herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 60/050,675
FILING DATE: 25-JUN-97
ATTORNEY/AGENT INFORMATION:
NAME: Petithory, Joanne R.
REGISTRATION NUMBER: P42,995
REFERENCE/DOCKET NUMBER: 2000-0455,390

```
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-324-0880
; TELEFAX: 650-324-0960
; TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2169 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-105-390-5

Query Match 1.5%; Score 73.2; DB 4; Length 2169;
Best Local Similarity 75.3%; Pred. No. 7.6e-08;
Matches 119; Conservative 0; Mismatches 33; Indels 6; Gaps 2;

QY 4375 TAGTAGCTATAAACCAGCTATAACATATTTAAAGAGATAAAGAGAGAGAGATAG 4434
Db 283 TATTAGCTATAAACCAGCTATAACATATTTAAAGAGATAAAGAGAGAGATAG 4434
QY 4435 CAGCGGCTATATTTAGCCAGCTACAGCAGGACTCAAGACGTA-----ATGTGT 4489
Db 342 CAGCGGCTACAGATTGTTAAACCACTACAGCAAGACTTTAAGATCAATGTGTATAA 401
QY 4490 GTATATGACAGTAGGACCAAGGATTAAAGATATAGTA 4527
Db 402 ATCTATGACAGTGGGACGAGCTTAATATATAATA 439

RESULT 8
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHRIEFINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-232-463-14
; IMMEDIATE SOURCE:
; CLONE: pTZgpt-Fis
; US-08-232-463-14

Query Match 1.4%; Score 70.6; DB 1; Length 7218;
Best Local Similarity 5.9%; Pred. No. 6.3e-07;
Matches 19; Conservative 194; Mismatches 108; Indels 0; Gaps 0;

QY 1001 GGAAAAAGAGTAGATGTAGATGTAGCAACAACAAGAGAGAGAGAGAGAGAT 1060
Db 1352 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1293
QY 1061 GCCAAGTGCACAAGTAAGCTAAACAATCTAGGCGAGCATTCATAGAGGTCAAGCTG 1120
Db 1292 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1233
QY 1121 TATTGATTGGAGAGATATGGATTGATAGAGAAAAAGAGAGATAATAAAGGATA 1180
Db 1232 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1173
QY 1181 ATACCTGTGATGAGAGAGAGTGTGGCATGGCGATCGCGCAGGTTGCGGACGACA 1240
Db 1172 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1113
QY 1241 TGCCATCGCGGCGGTACTCGCTTGGCTGCGCCACGCGACGCTGCTCTCCCTT 1300
Db 1112 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1053
QY 1301 GTACCAGAGAGACGCCGA 1321
Db 1052 CGACCTGCAAGCAAGCTCGGA 1032

RESULT 9
US-09-103-840A-2/c
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
; US-09-103-840A-2

Query Match 1.2%; Score 61; DB 4; Length 4403765;
Best Local Similarity 47.7%; Pred. No. 0.005;
Matches 244; Conservative 0; Mismatches 260; Indels 7; Gaps 2;

QY 1262 CGTTGGCTCGGCCACGCGACGCTGTCTCTCCCTGTGTACGAGGAGAGAGAGAG 1321
Db 3928207 CGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3928148
QY 1322 TGCAGCGCGCGCTCTCTGAGGCGGACCTCTGAGGCGGCGGAGAGATCGGAGT 1381
Db 3928147 CGAATCCGCGGCTTGCCTCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3928088
QY 1382 TGCCCTTGCCCGCAGTCGCGCATCTCTGCTGCCCGCGCGCGCGCGCGCGCGCG 1441
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QY 1604 GGGGAACCATCCGCTCCACTGG 1626
||| ||| ||| ||| |||
Db 498 GGACACCGGTGGGACGGGGG 520

RESULT 12
US-09-105-537-1/c
; Sequence 1, Application US/09105537A
; Patent No. 6265202
; GENERAL INFORMATION:
; APPLICANT: Sherman, D.H.
; APPLICANT: Liu, H.
; APPLICANT: Xue, Y.
; APPLICANT: Zhao, L.
; TITLE OF INVENTION: DNA encoding methymycin and pikromycin
; FILE REFERENCE: 600.4380S1
; CURRENT APPLICATION NUMBER: US/09/105,537A
; CURRENT FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 15872
; TYPE: DNA
; ORGANISM: Streptomyces venezuelae
US-09-105-537-1

Query Match 1.2%; Score 50.6; DB 4; Length 15872;
Best Local Similarity 45.5%; Pred. No. 0.00026;
Matches 216; Conservative 0; Mismatches 259; Indels 0; Gaps 0;

QY 1207 ATGGCGAGATCGGCGCAGGTTGGGACGAGCATGCCATCCGCGGGCGTACTCGTTG 1266
Db 5238 AGACACACGGGTGGTGTCGTTGAGCGGCGAGCGACCCTGCCTCTGACCCCTC 5179
QY 1267 GCGTCGCGCCCAGCGCAAGGTGTGCTCTCCCCCTGGTACCAGAGCACAGCCCGATCGG 1326
Db 5178 AGGGACTCGACGACCTCGGCCTCGCCGCTGTGACGCGCATCATCGCCGCCCTCGCGG 5119
QY 1327 CCGCGCGTCTGAGGGCGACCTTGAGCGGCGGACGAGATCGCGATAGAGTCGGTCC 1386
Db 5118 GCCGACTCATGACGGCGCGGGCGGTGACGAGAGTCTGCGCGTTCGTGAGGGGAGG 5059
QY 1387 TTGGCCCCAGTCGGCCATCTTGTTGGCGCCGACGCGCAGGGACGAGCCGATCACAGG 1446
Db 5058 ACACCGCGAGTCTGCGCGCGCATCTGCGCGACGAGTGGCCGTTGACAGTTCGGG 4999
QY 1447 AACTGGCGGAGCAGAGAGGGCGTTAGCGAAGGACATPCCCGGGACCGAGCCGACGTG 1506
Db 4998 ACGAGGCGGTGGTGTTCGAGAGGGCGGAAACAGCCCCACCTCGAAGGCGAAGAGGGCGGGC 4939
QY 1507 CGGTTGGAGTCGATCGCGCTGTGGAGCGGCTCTGTGGGCTCTCTCCATCGAGCTGCGGG 1566
Db 4938 TGGGTGTACGGGTGAGTCTCAGTCTCTCCCGCGCGGACGATPCCCGACGCGGGCGG 4879
QY 1567 GAGAGCGCGGAGTAGAGGGGTGGGGCGGCACATCCGGGGGGAACCATCGCTCCCACTGG 1626
Db 4878 TCAGAGTCAGGTCAGAGGGCGCGTACACGCTGTCAGGGGCGGCGGCAACACGSGGTGC 4819
QY 1627 GACCCCAACACGCCCCCGCCCCCGCATGTTCAGTTCGCTCCCAAGATGAACA 1681
Db 4818 GCGGCGCGCACTTCCTGTGCCATGTGGACGACGGGCTGCGCTCTCTTGGCGGTTGAACA 4764

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Barnes & Thornbury
STREET: 11 S Meridian
CITY: Indianapolis
STATE: Indiana
COUNTRY: USA
ZIP: 46204
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/728,956
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Breen, John P.
REGISTRATION NUMBER: 38,833
REFERENCE/DOCKET NUMBER: 3220-26119
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317)231-7745
TELEFAX: (317)231-7433
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1591 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Oryza sativa
US-08-728-956-3

Query Match 1.2%; Score 60.4; DB 1; Length 1591;
Best Local Similarity 54.7%; Pred. No. 7.8e-05;
Matches 163; Conservative 0; Mismatches 131; Indels 4; Gaps

QY 4132 AGTACTCCCTCCGTCCTCAAAATAAGTGTAGTTTGTAGCACATATTATGTCACAGCTTTGAC 4191
DB 723 AATACTCCCTCCGTTCCAAATGTTTGACACCGCTGATTTTTTTTGTATATGTTGAT 782
QY 4192 CATCTGCTCTATTGAAAGAAGATTATGATNAGTATTTTATTTATGTTATATAGATGATPAAA 4251
DB 783 CATTTGCTCTATTTCAAAATAATTAAGTATTTATTTATTTTCGTATCATCTTTGACTCAT 842
QY 4252 CATCAATAGTACTTTATGTGTGACTAAATTTTTTTTTTAATATTTTTTATTAATTTTTTCAA 4311
DB 843 GCTTAAATATATTTTCATGTCGCAC--ATATAGTTTTACATATTTTCACAAATTTTTTTGNA 900
QY 4312 TAAGACGGATGGTCAAGCGCTAAACATGGATATCTATGGCTACACTATTTTGTGGACGG 4371
DB 901 TAAGACGAACGGTCAAA--CATGTGCTAAAAAATAAAGGTGTCAAAATTTTGTGAACCG 958
QY 4372 AGGTAGTAGGCTATAAACACCATTAACATATTTTAAAGAGATTAAGAGAGAGAGAG 4429
DB 959 AGGGAGTATCTCTATATATATGCAGATCGGGAGTCGGGAATACATCAAGACCGGAGTG 1016

RESULT 14
US-09-197-649-7
; Sequence 7, Application US/09197649
; Patent No. 6194550
; GENERAL INFORMATION:
; APPLICANT: Gold, Larry
; APPLICANT: Tuerk, Craig
; APPLICANT: Pribnow, David
; APPLICANT: Smith, Jonathan D.
; TITLE OF INVENTION: Systematic Polypeptide Evolution by Reverse Translat
; FILE REFERENCE: NE02/C1-CON
; CURRENT APPLICATION NUMBER: US/09/197,649

```



```
/ CURRENT FILING DATE: 1998-11-23
/ EARLIER APPLICATION NUMBER: 07/829,461
/ EARLIER FILING DATE: 1992-01-31
/ EARLIER APPLICATION NUMBER: 07/739,055
/ EARLIER FILING DATE: 1991-08-01
/ EARLIER APPLICATION NUMBER: 07/561,968
/ EARLIER FILING DATE: 1990-08-02
/ NUMBER OF SEQ ID NOS: 26
/ SOFTWARE: Patent In Ver. 2.0
/ SEQ ID NO 7
/ LENGTH: 390
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Sequence
/ OTHER INFORMATION: having a 120 repeat of ACG flanked by fixed
/ OTHER INFORMATION: fragments having NcoI restriction sites.
US-09-197-649-7

Query Match      1.2%; Score 60; DB 4; Length 390;
Best Local Similarity 48.0%; Pred. No. 4.4e-05;
Matches 171; Conservative 0; Mismatches 185; Indels 0; Gaps 0;

QY 1183 ACCGTGATGAGGAGAGGTGGCATGCGGATCGGCGGAGCTTCGGACGAGCATG 1242
Db 31 ACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 90

QY 1243 GCCATCCGGCGGCGCTACTCTGTCGTCGCGCCGACGACGACGACGACGACG 1302
Db 91 ACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 150

QY 1303 TACCAGAGGACACGCGGATGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 1362
Db 151 ACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 210

QY 1363 AGATCGAGTAGAGGTGCGTCTGTCGTCGTCGTCGTCGTCGTCGTCGTCG 1422
Db 211 ACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 270

QY 1423 CAGGGGACGAGCGCGATACAGGAACTGCGCGGAGGAGGCGGTTAGCGAAG 1482
Db 271 ACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 330

QY 1483 ATCCGGGACGACGCGCGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1538
Db 331 ACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 386

RESULT 15
US-08-858-003-1/c
/ Sequence 1, Application US/08858003
/ Patent No. 6060234
/ GENERAL INFORMATION:
/ APPLICANT: Katz, Leonard
/ APPLICANT: Stassi, Diane L.
/ APPLICANT: Summers Jr., Richard G.
/ APPLICANT: Ruan, Xiaolan
/ APPLICANT: Pereda-Lopez, Ana
/ APPLICANT: Kakavas, Stephan J.
/ TITLE OF INVENTION: NOVEL POLYKETIDE DERIVATIVES
/ NUMBER OF SEQUENCES: 34
/ CORRESPONDENCE ADDRESS:
/ ADDRESS: 100 Abbott Laboratories
/ CITY: Abbott Park
/ STATE: Illinois
/ COUNTRY: USA
/ ZIP: 60064-3500
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
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/ SOFTWARE: FastSeq Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/858,003
/ FILING DATE: 16-MAY-1979
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Dianne Casuto
/ REGISTRATION NUMBER: P-40,943
/ REFERENCE/DOCKET NUMBER: 4952.US.P2
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (847)-938-3137
/ TELEFAX: (847)-938-2623
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 925 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: linear
/ US-08-858-003-1

Query Match      1.2%; Score 60; DB 3; Length 925;
Best Local Similarity 47.2%; Pred. No. 7.2e-05;
Matches 183; Conservative 0; Mismatches 205; Indels 0; Gaps 0;

QY 1240 ATGGCCATCCGCGGCGCTACTCTGTCGTCGTCGTCGTCGTCGTCGTCGTC 1299
Db 707 ATGCGCTGCTGTCGAGTGTGGTGGAGGTGTCTGTCGTCGTCGTCGTCGTCG 648

QY 1300 TGTATACAGAGACAGCGCGCATCGGCGCGCGCGCTCTCGAGGGCGACCC 1359
Db 647 TGGTCCAGTGGTGTGTGTCGCGGCTGGTGTGTCGTCGTCGTCGTCGTCGTC 588

QY 1360 ACGAGATCGGAGTAGAGTTCGCTGTCGTCGTCGTCGTCGTCGTCGTCGTC 1419
Db 587 GTGTGTCGCGGCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTC 528

QY 1420 GCGCAGGGGACGAGCGCGCATGACAGGAACTGTCGCGGACCGAAGAGGG 1479
Db 527 TGGTGGCGATGTGTGAGGAGTGTGTCGTCGTCGTCGTCGTCGTCGTCGTCG 468

QY 1480 GACATCCCGGACCGACCCCGAGTTCGCTGTCGTCGTCGTCGTCGTCGTCG 1539
Db 467 TTGATGCGCGCATGAGATGTGTCTGTCGTCGTCGTCGTCGTCGTCGTCGTCG 408

QY 1540 TGGGCTCTCTCCCATCGGAGTTCGCGGAGAGGCGGAGGATGGAGGGTTGG 1599
Db 407 GGTGTCGTGCGGACGCGGAGCATGCGCGCGCGGCGGCGAGTTTTCATGAG 348

QY 1600 TCCGGGGGAACCATGCGTCGCCAGTGGG 1627
Db 347 CGTGTGTGACGAGGTGGACGCGCTCGG 320

Search completed: March 26, 2003, 18:50:29
Job time : 20400.7 secs
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Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	121.8	2.4	5757	10	US-09-993-170-56	Sequence 56, Appl	
2	118.4	2.4	949	10	US-09-770-445-342	Sequence 342, Appl	
C 3	114.4	2.3	547	9	US-10-101-464-374	Sequence 374, Appl	
C 4	114.2	2.2	2000	10	US-09-887-576-870	Sequence 870, Appl	
5	83.2	1.7	2000	10	US-09-887-576-859	Sequence 859, Appl	
6	68.2	1.4	520	9	US-10-184-644-332	Sequence 332, Appl	
7	61	1.2	863	10	US-09-974-300-5249	Sequence 5249, Appl	
C 8	60.6	1.2	15872	9	US-09-860-046-1	Sequence 1, Appl	
C 9	60.5	1.2	15872	10	US-09-861-286-1	Sequence 1, Appl	
C 10	60	1.2	390	10	US-09-790-399-7	Sequence 7, Appl	
C 11	60	1.2	925	9	US-09-735-056-1	Sequence 1, Appl	
C 12	58	1.2	615	9	US-10-125-815-4	Sequence 4, Appl	
C 13	57.4	1.1	2010	12	US-10-032-717-9	Sequence 9, Appl	
C 14	56.4	1.1	405	10	US-09-878-574-3891	Sequence 3891, Appl	
C 15	55.2	1.1	2087	10	US-09-349-385-11	Sequence 11, Appl	
16	54	1.1	264	10	US-09-969-373-472	Sequence 472, Appl	
17	54	1.1	2000	10	US-09-887-576-832	Sequence 832, Appl	
C 18	53.2	1.1	4689	9	US-09-860-046-34	Sequence 34, Appl	
C 19	53.2	1.1	4689	10	US-09-861-289-34	Sequence 34, Appl	

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 342
; LENGTH: 949
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-770-445-342

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RESULTS AND DISCUSSION

RESULT 4
US-09-887-576-870/c

```

RESULT 5
US/09-887-576-859
  Sequence 859, Application US/09887576
  Patent No. US2002014047A1
  GENERAL INFORMATION:
  APPLICANT: Budworth, P.
  APPLICANT: Brown, D.
  APPLICANT: Chang, H.
  APPLICANT: Zhu, T.
  APPLICANT: Han, B.
  APPLICANT: Wang, X.
  APPLICANT: Cooper, Bret
  TITLE OF INVENTION: Promoters for re
  FILE REFERENCE: 1360.001US1
  CURRENT APPLICATION NUMBER: US/09/887
  CURRENT FILING DATE: 2001-06-25
  PRIOR APPLICATION NUMBER: US 60/213,
  PRIOR FILING DATE: 2000-06-23
  PRIOR APPLICATION NUMBER: US 60/214,
  PRIOR FILING DATE: 2000-06-23
  PRIOR APPLICATION NUMBER: US 60/258,
  PRIOR FILING DATE: 2000-12-29
  NUMBER OF SEQ ID NOS: 875
  SOFTWARE: FastSeq for Windows Version

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RESULT 6
US-10-184-644-332
; Sequence 332, Application US/10184644
; Publication No. US20030044930A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: ACID-SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C237
; CURRENT APPLICATION NUMBER: US/10/184.644
; CURRENT FILING DATE: 2002-06-28
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 332
; LENGTH: 520
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-184-644-332

Query Match 1.4%; Score 68.2; DB 9; Length 520;
Best Local Similarity 20.1%; Pred No. 3.2e-07;
Matches 88; Conservative 91; Mismatches 259; Indels 0; Gaps

QY 1086 AATCTAGGCGAGCATTCGATAGAAGTCAGCGTGTATTGATGGAGAGATATGGATTG 1145
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 1 MNKKILKDELLSETQAAFHQIAEMPEINVPKRRRNGVNSLAVVYVILLTAGA 60

QY 1146 ATAGAGAAAAGACAGAAATATATATAGGAGATATACCTGATGAGAGAGAGAGTGGG 1205
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 61 GLLVVVNLNQARLRVLEWYFLNDYTLAAEDSPFSLLQSAHPGEHLAQAGASRLQVLAOL 120

QY 1206 CATGGCGAGATCGGCGCGAGTTGCGGACGAGCATGCCATCCGCGGCGCTACTCGTT 1265
   :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: :: ::
Db 121 TWRVRSVHLLQKVNDFONTNPGMFR1KGQGAPGLQHGKGMGNFGAPGPPPPPAEKGA 180

QY 1266 GGCCTCGGCCGACGCGAGCGTGTGCTCTCCCTCGTTACGAGAGCAGCGCGCATGCG 1325

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Db 181 GAMRGDAGTGPSPGPPGVKRGALQPGAPKQAGATGTPPGVKGSKGDGLGPK 240
QY 1326 GCCCGCGGTCTCGAGGCGACCCCTGAGCGCGGACGAGATCGGAGTAGAGTCTGCTGCC 1385
Db 241 GETCTGKEKGDGLGLPSKGRDMKGDAGVMGPPGAQSGKGDGRPPGGLGFPFKAQKDQ 300
QY 1386 CTTGGCCAGTGGCCATCTCTGTCGCCCGACGCGCGAGGGAGCGGATGACAGG 1445
Db 301 GQPLQGVTPPPGAVHFGAKGPGSAGSPRAGLPGSPGSPGATGLKSGKDTGLQGGQ 360
QY 1446 GAACTGGCGGAGCGAAGAGGCGGCTTACGAAGACATCCCGGAGCGGACGCGGAGGT 1505
Db 361 GKESGVPAGVKGEGSPGLAGPKGAPQAQKQDQGVKSGSGEQGVKGEKGERGEN 420
QY 1506 GCGTTGGAGTCATGCC 1523
Db 421 SVSVRIWGSNRRGAEVY 438

RESULT 7
US-09-974-300-5249
; Sequence 5249, Application US/09974300
; Patent No. US20020146721A1
; GENERAL INFORMATION:
; APPLICANT: Berka, Randy M.
; APPLICANT: Clausen, Ib Groth
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; TITLE OF INVENTION: Expression
; FILE REFERENCE: 10085-500-US
; CURRENT APPLICATION NUMBER: US/09/974,300
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 09/680,598
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/279,526
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 8481
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5249
; LENGTH: 863
; TYPE: DNA
; ORGANISM: Bacillus clausii
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(863)
; OTHER INFORMATION: n = A,T,C or G
US-09-974-300-5249

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Query Match	1.2%;	Score 61;	DB 10;	Length 863;	
Best Local Similarity	49.0%;	Match No. 3.3e-05;			
Matches 216;	Conservative	0;	Mismatches 219;	Indels 6;	Gaps 12;
QY 1208	TGCGGAGATCGCGCGCAGGTTCGGGACGACGATGGCCATCCGGCGGGCGTACTCTGTGG	1267			
Db 213	TGACCGGACGCCGATGCGCGGATCGGACGCCGACGGCGGATGCCGATGCCGACGC	272			
QY 1268	CGTCGGCCACGACGGTGTGCTCTCTCCCTCGTACCAGAGGACACGCCGATGCGGC	1327			
Db 273	GGACGCTGATCCGACGCTGATCTCACGC--GATGCCGACGCCGCGGATGGCGGA	329			
QY 1328	CGCGGGTCTCGAGGGCGACCTCGGACGGCGGACGATGCGAGTAGAGCTCGTGCCCT	1387			
Db 330	TGCGGACGCCGATCCGACGCTGAOCGCGATGCGGATGCGGACGGCGGATGCGGACGCCGA	389			
QY 1388	TGCCCCACTCGCGCCATCCTGTGTCGCCGCGACGGCGCAGGGGACGGCCGATGACAGGGA	1447			
Db 390	TGCGGACGCTACGCTGACCTGATGCCGATGCCGATGCGGATGCGGATGCGGACGCCGA	449			
QY 1448	ACTGTCCGAGCGAAGGAGGGCGTTAGCGAAGGACATCCCGGACCGACGCCGCGAGTGC	1507			
Db 450	TGCNGATGGGATTGCGACGCCGATGCCGATGCCGATGCCGACGCCGATGCGGACGCTGA	509			
QY 1508	GTTGGAGTTCGATCCGTTGTGGAGCGGCTGTGGGCGCTCCTCC--ATCGGAGCTGGC	1564			

Db	510	TGCTGACGGGATCCGATCCGATGCGGATGCGGACGCCGATGCGGATGCGGATTCGGA	569
Qy	1565	GGGAGAGCGGAGGATGGAGGGTTGGGGGGGCGACTCCGGGGGAACCATGCGGTCGCA	1624
Db	570	CGCTGATCGGANGCCGATCGGATGCTGACGCGGACGCGATGCGATGCGACGCTGA	629
Qy	1525	GGGACCCCAACGCCCCCGC	1645
Db	630	CGCTGATCCGATCGCNGACG	650

RESULT 8
 US-09-860-846-1/C
 ; Sequence 1, Application US/09860846
 ; Patent No. US20020164742A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Sherman, D.H.
 ; APPLICANT: Liu, H.
 ; APPLICANT: Xue, Y.
 ; APPLICANT: Zhao, L.
 ; TITLE OF INVENTION: DNA encoding methymycin and pikromycin
 ; FILE REFERENCE: 600.4380S1
 ; CURRENT APPLICATION NUMBER: US/09/860,846
 ; CURRENT FILING DATE: 2001-05-18
 ; PRIOR APPLICATION NUMBER: 09/105,537
 ; PRIOR FILING DATE: 1998-06-26
 ; NUMBER OF SEQ ID NOS: 43
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 1
 ; LENGTH: 15872
 ; TYPE: DNA
 ; ORGANISM: Streptomyces venezuelae
 US-09-860-846-1

Query Match	1.2%	Score 60.6;	DB 9;	Length 15872;
Best Local Similarity	45.5%;	Prod. No. 0.00039;		
Matches 216;	Conservative 0;	Mismatches 259;	Indels 0;	Gaps 0

Qy	1207	ATGGCGAGATCGGGCGCAGGTTGCGGACGAGCATGCCATCGGGGGCGCTACTCGTTG	1266
Db	5238	ACGACCACGGCGGTGGTCTGTTGACGGGGGACGGACCTGCCCTCGTAGCCCTTC	5179
Qy	1267	GCCTGGGCCACGGACAGTGTGCTCTCCCTCGTGTACAGAGGACACGGCCGATGGG	1326
Db	5178	AGGGACTCGACGACCTCGGCTCGCCGCTCGACGGCGATCATCGCGCCGCTCGGG	5119
Qy	1327	CGCGCGTCTGACGGGCGACCTTGAGCGGGCGACAGATCGGAGTAGAGTCGCTGCC	1386
Db	5118	GCCGACTGATGACCGCGCGCGGGTGTACGAGACGTGCGGCTCTGTGAGGGAGAGG	5059
Qy	1387	TTGGCCCATGTGGCCATCCTGTGTCCCGACGGCGAGGGACAGAGCCGATGACAGG	1446
Db	5058	ACACCGGCGACGTGCGGGGGGGGATCTCGCGACGAGTGGCGGTGACGAGTTCGGG	4999
Qy	1447	AACTGGCGGAGCAAGAGGGGGTTAGGAGAGGACATCCCGGGACCGACGCCGAGGTG	1506
Db	4998	ACAGAGCCTGTGTGTTGAGAGGCGGGAACACGCCACCTCGAGGCGAGAGCGCGGC	4939
Qy	1507	CGTGTGGAGTCGATGCCGTTGTGAGCGGCTGTGGGCGGCTCTCCCATCGGAGCTGGG	1566
Db	4938	TGGGTGTACGGGTGAGTCCAGCTCTCCCGGGCGGACGATCTCCCGACAGCGGCGG	4879
Qy	1567	GAGAGCGAGATGAGGGGTTGGGGGCGACATCCGGGGGAACCATGCGCTCCCATGG	1626
Db	4878	TCGAGGTGACGTTGAGGCGCGGTACAGGTGTGAGAGGGCGGCGGCAACACGGGTGC	4819
Qy	1627	GAGCCCAACACGCCCGCGCCGCCATGTTTCGACTCCCTCCAGGATGAACA	1681
Db	4818	CGGCGCGCAGTTCTCGCCCATGGGCGAGCGCTGCGCTCCCTCGCGCGGTGACA	4764

RESULT 9

RESULT 9

```
US-09-861-289-1/c
; Sequence 1, Application US/09861289
; Patent No. US20020110897A1
; GENERAL INFORMATION:
; APPLICANT: Sherman, D.H.
; APPLICANT: Liu, H.
; APPLICANT: Xue, Y.
; APPLICANT: Zhao, L.
; TITLE OF INVENTION: DNA encoding methymycin and pikromycin
; FILE REFERENCE: 600.438US1
; CURRENT APPLICATION NUMBER: US/09/861,289
; CURRENT FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: 09/105,537
; PRIOR FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 15872
; TYPE: DNA
; ORGANISM: Streptomyces venezuelae
US-09-861-289-1

Query Match      1.2%; Score 60.6; DB 10; Length 15872;
Best Local Similarity 45.5%; Pred. No. 0.00039;
Matches 216; Conservative 0; Mismatches 259; Indels 0; Gaps 0;

QY 1207 ATGGCGAGATCGCGCGGAGGTTCGGGACGAGCATGGCCATCCGGGGGGCTACTCGTTG 1266
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5238 ACGACACGCGGTGGTGGTCCGTGAGCGGGCGGACGGCGACCCCTCGTCGTAGCCCTTC 5179
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1267 GCGTCGGCCAGCGCGACGCTGTCGCTCTCCCTTGTACAGAGGACACGCCCGCATCGG 1326
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5178 AGGGACTCGACGACCTCGSCCTCGCCCTGCAAGCGCATCATCGCCCGCCCTCGCGG 5119
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1327 CGCGCGGTCTCGAGGCGGACCCCTGAGGCGGCGACGAGATCGGAGTAGAGTTCGGTCCC 1386
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5118 GCCAGCTGCATGACGCGCGCGCGCGGTGACGAGAGCTGCGCGCTCGTCGAGGGAGAGG 5059
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1387 TTGGCCAGTCGCGCCATCTGCTGTCGCGCGCGCGCGCGGACGAGCGCATCACAGGG 1446
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 5058 ACACGGCGACGTGCGCGCGCGCGGTCTGCGCGAGGATGCGCGGTGAGCAGGTTCGGGG 4999
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1447 AACTGGCCGAGGAGGAGGCGCTTAGCGAAGGACATCCCGGGACCGACGCCAGGTG 1506
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 4998 ACGAGGCGGTGTTTCGAGGAGGGGGAACAGGCCACCTCGAAGGCGAAGGCGGGG 4939
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1507 CGGTGAGTCGATCCGCTTGTGAGCGGCTCTGCGGCTCTCCCATCGAGTCCGGG 1566
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 4938 TGGGTGTACGCGGTGAGGTCCAGCTCTCCCGCGCGCGACGATCTCCCGACGCGCGG 4879
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1567 GAGAGCGGAGGATGAGGGGTTCGGGCGCGCATCTCCGGGGGACCATCGCTCCCATGG 1626
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 4878 TCGAGGTGACGTTCGAGGCGCGGTACACGCTGTCGAGGCGCGCGGCGAACAACGGGTGC 4819
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1627 GACCCGACACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1681
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 4818 GCGGCGCGCATCTCTCCGCCCATCGCGAGCGGCTGCGCTCCCTGCGCGGTGAACA 4764
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 10
US-09-790-399-7
; Sequence 7, Application US/09790399
; Patent No. US20020038000A1
; GENERAL INFORMATION:
; APPLICANT: Gold, Larry
; APPLICANT: Turk, Craig
; APPLICANT: Fribnow, David
; APPLICANT: Smith, Jonathan D.
; TITLE OF INVENTION: Systematic Polypeptide Evolution by Reverse Translation
; FILE REFERENCE: NEX02/c1-CON2
; CURRENT APPLICATION NUMBER: US/09/790,399
; CURRENT FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 09/197,649
```

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; PRIOR FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: 07/829,461
; PRIOR FILING DATE: 1992-01-31
; PRIOR APPLICATION NUMBER: 07/739,055
; PRIOR FILING DATE: 1991-08-01
; PRIOR APPLICATION NUMBER: 07/561,968
; PRIOR FILING DATE: 1990-08-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 390
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Sequence
; OTHER INFORMATION: having a 120 repeat of ACG flanked by fixed
; OTHER INFORMATION: fragments having NcoI restriction sites.
US-09-790-399-7

Query Match      1.2%; Score 60; DB 10; Length 390;
Best Local Similarity 48.0%; Pred. No. 3.3e-05;
Matches 171; Conservative 0; Mismatches 185; Indels 0; Gaps 0;

QY 1183 ACTGTGATGAGGAGAGGTGTGGCATGGCGGATCGCGCGAGGTTGCGGACGAGCATG 1242
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 31  ACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 90
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1243 GCCATCGGGGGGGTACTTCGTTGGCTTCGGCCCGACGCGACGCGTGTGCTCTCCCTCG 1302
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 91  ACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 150
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1303 TACCAGAGGACGCGCCGATCGCGCGCGGCTCTCGAGGGGCGCCCTGAGCGCGGAGG 1362
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 151 ACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 210
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1363 AGATTCGAGTGTAGAGTTCGTCCTTGGCCCGAGTCGCGCATCTGTGCGCGCGAGGGG 1422
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 211 ACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 270
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1423 CAGGGGACGAGGCGGATGACAGGGAACGTGCGCGGACGAGGAGGCGGTAGCGAGGAC 1482
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 271 ACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 330
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1483 ATCCGCGGACGACGCGCGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1538
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 331 ACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACGACG 386
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 11
US-09-735-056-1/c
; Sequence 1, Application US/09735056
; Publication No. US20030013662A1
; GENERAL INFORMATION:
; APPLICANT: Katz, Leonard
; APPLICANT: Stassi, Diane L.
; APPLICANT: Summers Jr., Richard G.
; APPLICANT: Ruan, Xiaolan
; APPLICANT: Pereda-Lopez, Ana
; APPLICANT: Kakavas, Stephan J.
; TITLE OF INVENTION: NOVEL POLYPEPTIDE DERIVATIVES
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Rd.
; CITY: Abbott Park
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
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; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION NUMBER: 60/158,305
; APPLICATION NUMBER: 60/158,305
; FILING DATE: 1999-10-08
; CLASSIFICATION: US/09/735,056
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/858,003
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: biane Casuto
; REGISTRATION NUMBER: P-40,943
; REFERENCE/DOCKET NUMBER: 4952.US.P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (847)-938-3137
; TELEFAX: (847)-938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 925 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-09-735-056-1

Query Match 1.2%; Score 60; DB 9; Length 925;
Best Local Similarity 47.2%; Pred. No. 6.4e-05;
Matches 183; Conservative 0; Mismatches 205; Indels 0; Gaps 0;
QY 1240 ATGGCCATCCGGGGGCTACTGTTGGCGTCCGCCAGCCAGCGGCTGCTCTCCCGC 1299
Db 707 ATCCCGTGTGTGAGGTGGTGGAGGTGTCGGTGTAGCGGACGGTGGCGTGTGATGTC 648
QY 1300 TGGTACAGAGACAGCCGATCGCGCCGCGTCTCGAGGCGGACCTCGAGCGGGCG 1359
Db 647 TGGGTCCAGTGGTGTGCGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 588
QY 1360 ACAGATCGGATAGAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1419
Db 587 GTGTGTGGGGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 528
QY 1420 GCGCAGGGACGAGCGGATGACAGGAGAACTGGCCGCGAGCGAGGCGGTTAGCGAAG 1479
Db 527 TGGGTGGCATGTGTGAGGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 468
QY 1480 GACATCCCGGACAGCCGCGAGGTGGGTGGATGCGATGCGTGTGGAGCGGCTCG 1539
Db 467 TTGATGGCGGATGAGATGGTGTGCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 408
QY 1540 TGGGCGCTCTCCATCGGAGTGGCGGAGAGCGGAGGATGGAGGTTGGGGCGGCAC 1599
Db 407 GGTGCGTGGCGAGCGGCGAGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 348
QY 1600 TCCGGGGGAACCATCCGCTCCCATGGG 1627
Db 347 CGTGTGTGACGAGGTGGACGGCTGG 320

RESULT 12

US-10-125-815-4/c
; Sequence 4, Application US/10125815
; Patent No. US20020173008A1
; GENERAL INFORMATION:
; APPLICANT: Hu, Zhihao
; APPLICANT: McDaniel, Robert
; APPLICANT: Santi, Daniel V.
; TITLE OF INVENTION: RECOMBINANT POLYKETIDE SYNTHASE GENES
; FILE REFERENCE: 300622004720
; CURRENT APPLICATION NUMBER: US/10/125,815
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 09/679,279
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: 60/190,024
; PRIOR FILING DATE: 2000-03-17

; PRIOR APPLICATION NUMBER: 60/158,305
; PRIOR FILING DATE: 1999-10-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 615
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: megKS6
; US-10-125-815-4

Query Match 1.2%; Score 58; DB 9; Length 615;
Best Local Similarity 48.2%; Pred. No. 0.00015;
Matches 163; Conservative 0; Mismatches 175; Indels 0; Gaps 0;

QY 1316 CCGCATGCGGCGCGCGCTCGAGGGGACCCCTGGAGCGCGGAGATCGAGTAGA 1375
Db 498 CGCGCGCGCGCGCGCGCTCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 439
QY 1376 GGTGCGTGTGCGCGCGCGCTCGAGGGGACCTCGAGGGGCGCGCGCGCGCGCG 1435
Db 438 CCAGCGCGCGCGCGCGCTCGAGGGGCGCGCGCGCGCGCGCGCGCGCGCGCG 379
QY 1436 CGATGACAGGAACTGCGCGGAGCGAGGAGGCGTTAGCGAGGACATCCCGGAG 1495
Db 378 CGACCGCGCGCGCGCGCGCTCGAGGGGCGCGCGCGCGCGCGCGCGCGCGCG 319
QY 1496 CGCCCGAGTGGGTGGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 1555
Db 318 CTGAGCGTGGCGCGCGCTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 259
QY 1556 GGAGTGGCGGCGGAGCGGAGGAGTGGAGGCGCGCGCGCGCGCGCGCGCGCGCG 1615
Db 258 GCGCGAGCGCGCTAGCTGCGCGAGGCGCGCGCGCGCGCGCGCGCGCGCGCG 199
QY 1616 CGTCCCGTGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1653
Db 198 CGGTGCG 161

RESULT 13

US-10-032-717-9/c
; Sequence 9, Application US/10032717
; Patent No. US20020151709A1
; GENERAL INFORMATION:
; APPLICANT: Andre R. Abad
; APPLICANT: Nicholas B. Duck
; APPLICANT: Xiang Feng
; APPLICANT: Ronald D. Flanagan
; APPLICANT: Theodore W. Kahn
; APPLICANT: Lynn E. Sims
; TITLE OF INVENTION: Genes Encoding No. US20020151709A1 Proteins With
; FILE REFERENCE: 35718/237005
; CURRENT APPLICATION NUMBER: US/10/032,717
; CURRENT FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 60/242,838
; PRIOR FILING DATE: 2000-10-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 2010
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2010)
; OTHER INFORMATION: Maize optimized Cry1218-1
; NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: mo1218-1
; US-10-032-717-9

Query Match 1.1%; Score 57.4; DB 12; Length 2010;
Best Local Similarity 44.5%; Pred. No. 0.00054;
Matches 229; Conservative 0; Mismatches 286; Indels 0; Gaps 0;

QY 1208 TGCGAGATCGCGCGCAGGTGTCGACGACGATGCGCATCCGCGCGCGTACTCGTTGG 1267
DB 862 TGGGAAGAGGCCACACCGTCGAGCACGCGGAGGATCATCTCCGCGCGAATGTTGT 803
QY 1268 CGTCGCCCGACGCGCAGGTGTCGCTTCGCCCTTGTACGAGGACGACGCGATCGCGC 1327
DB 802 AGTCCACCCACTGCTTGGCGGAGTGCCTTGAGCTTGGCGAGCGGTCTCATACCACT 743
QY 1328 CGCGGCTCTCGAGGCGGACCTCGAGCGCGGACGAGATCGGATAGATCGGTGCCCT 1387
DB 742 TCAGGAGTGGTTCGAGTACTCGCGGTGAGTTTCATCTGCGCTGCTAGTAGTTTGA 683
QY 1388 TGCCCCAGTCGCCCATCTCGTCCGCGCGACGCGCGAGGACGCGCATGACAGGA 1447
DB 682 TGTGTGTGTGACACGCGCCNCTCTCCCGAAGATGGAGCGTCTTGGAGGAGGA 623
QY 1448 ACTGCGCGGAGGACGAGGCGGTAGCGAAGACATCCCGGGACCGACCGCGAGTGC 1507
DB 622 GGTGGAGGTGCGCGCCATGCGCTTACACGCTGAGGAAGGCGACCTCGAAGTTGTCACGC 563
QY 1508 GPTTGGATCGATCGCTGTGAGCGGCTCGTGGGCGCTCTCCATCGGAGCTCGGGG 1567
DB 562 GGAAGAGGCGATGACTTGGTGAAGAGGAGTCGAGATCTGAAGCGGTTGCGCAGGT 503
QY 1568 AGAGCGGAGGATGAGGCGGTGCGGCGCACTCCGCGGGGAACCATCCCTCCAGTGG 1627
DB 502 CGCGGAGGCGCGGCGCGCTTGGGTTCTCTCCCACTCTCCAGGCGGTGAGTAGA 443
QY 1628 ACCCGACACGCGCGCGCGCGCGCTGTCGATGCGCTCCCGAGATGAACACCACT 1687
DB 442 GCTGTPAGTGTTCGCGAGCGCGCTCCAGCTCGGAGAGGCGCTTGTTCGCGGCGTACTCGG 383
QY 1688 TGTTCACGAGGAGGAGGACACGCGCGCGCGCC 1722
DB 382 CGATCTCTGCTGTGATGAGCTCTCCACTGCTCC 348

RESULT 14
US-09-878-574-3891/c
; Sequence 3891, Application US/09878574
; Patent No. US20020110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE OF INVENTION: Plants
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/333,535
; PRIOR FILING DATE: 1999-06-14
; NUMBER OF SEQ ID NOS: 15775
; SEQ ID NO 3891
; LENGTH: 405
; TYPE: DNA
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: LIB3028-004-Q1-B1-E11
US-09-878-574-3891

Query Match 1.1%; Score 56.4; DB 10; Length 405;
Best Local Similarity 47.5%; Pred. No. 0.00029;
Matches 166; Conservative 0; Mismatches 186; Indels 0; Gaps 0;

QY 1243 GCATCCGCGGCGTACTCGTTGGCGCGCGACGCGTGTGCTCTCCCGCTGG 1302
DB 405 GCTAGCACGAGGAGAAACCGCGGAGCGGTAGGAACCTTGACGGATTTCGCGCGG 346

QY 1303 TACCAGAGACACGCGCATCGCGCGCGCTCTCGAGGCGACCCCTGGAGCGCGCGAGC 1362
DB 345 TTCGATCGAGGCGGAGTCCGAGGAGATGATGCGGATGCCACCAAGGACGAACATGAAT 286
QY 1363 AGATCGGAGTAGAGTGGTCCCTTGGCCCATGTCGGCCATCTCTGTGCGCGCGACGCGC 1422
DB 285 CCGAGGAGAGGCGCTCGATGATGCTACTGCGCGTTGACGCGCGCGGACATGAAGAGCG 226
QY 1423 CAGGGAGCAGGCGCATGACAGAGAACTGCGCGGAGCGAAGAGGCGGTTAGCGAAGAC 1482
DB 225 GCGCGAGCGCGCGCTGTAGGGTCTCTGAGTGGAGCGGATGCGCGGGGCTCGACGATG 166
QY 1483 ATCCCGGAGCGACCGCGCGCGAGTGGGTTGGAGTGCATGCCGTTGTGGAGCGCTCGTGG 1542
DB 165 ATCTGTAACAATCGCGGAGCGACCATGAAGTAGGTGAGGAGGAGGAGGCGAAGAGC 106
QY 1543 GCCTCTCTCCATCGGAGTCCGCGGAGCGGAGGATGAGGCGGTTGGGGCG 1596
DB 105 GCGTTCGGGAGGCGGAGGTGAAGAGGAGAACTTGAGCGCGGAGCGAGAGGG 52

RESULT 15
US-09-349-385-11/c
; Sequence 11, Application US/09349385
; Patent No. US20020152495A1
; GENERAL INFORMATION:
; APPLICANT: Ito, Toshiro
; APPLICANT: Fromm, Michael
; APPLICANT: Meyerowitz, Elliot
; TITLE OF INVENTION: PLANTS HAVING SEEDLESS FRUIT
; FILE REFERENCE: MBI-0002
; CURRENT APPLICATION NUMBER: US/09/349,385
; CURRENT FILING DATE: 1999-07-09
; EARLIER APPLICATION NUMBER: 60/115,967
; EARLIER FILING DATE: 1999-01-15
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 2087
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: CDNA
US-09-349-385-11

Query Match 1.1%; Score 55.2; DB 10; Length 2087;
Best Local Similarity 44.9%; Pred. No. 0.002;
Matches 210; Conservative 0; Mismatches 258; Indels 0; Gaps 0;

QY 1194 GAGAAGGTGTGCGATGCGGAGATCGCGCGCAGGTTCGGAGCAGCATGCCATCCCGCG 1253
DB 1069 GAGATGGCGACCATGCTGCTCGCGCGAGCTCTCTCACCTCTGAGGAGGAGGAGC 1010
QY 1254 GCGGTACTGTTGGCGTTCGCGCGCAGCGCAGGTGCTCTCCCGCTTGTGTACGAGGAC 1313
DB 1009 GTCGAGAGTCAAGTTCGTTGAGGCGCGGAGTTTGGCGCGCGCGCTGCTC 950
QY 1314 AGCGCGGATGCGCGCGCTCTCGAGGCGCGCTGAGGCGCGCGCTGAGGCGGAGAGTCGAGTA 1373
DB 949 GTCGATGACGCCACGCGACGAAGTCTGGACCGCGCGCAGGACGCGCGCGGT 890
QY 1374 GAGTCTGCTGCCCTTGGCCCATGCTGCTGCTGCGCGCGCGCGCGCGCGAG 1433
DB 889 GACGTTGCTTGGTCTGACAGTTCGCGCGAGCGAGGAGTGTCTCGGACCATGTAAGGC 830
QY 1434 GCGATGACAGGAACTGCGCGCGAGGAGGAGCGGCTTACGAGGACATCCCGGAC 1493
DB 829 GCGGAGGAGTCAAGCCCTCGCGCGACCATGCTCTGAGATGCTCGGCTTCGCGCGCGC 770
QY 1494 GAGCGCGAGGTGCGGTTGAGTCTGCTGCTGAGGCGGCTGCTGCGGCTTCCTCCA 1553
DB 769 GCGCGCTGATGTGAGCTGCTACCGCGTGCAGGAGCGCTGCCATGATGTTGTGAGAGC 710

QY 1554 TCGAGCTCCGGGAGAGCGGAGGATGGAGGGTTGGGGCGCACTCCGGGGGAACCAT 1613
 Db 709 GCGGCGCTGGAGGTCCGGGCGGAGGCGACGGCGCCAGAGCGCACTGTTCGGCGGCGAT 650
 QY 1614 GCGGTCCAGTGGGACCCACACGCGCCCGCGCCCGCCCATGTCGA 1661
 Db 649 GAGCGGAGCATGGCCTCCGCTCACCTTGGGCTCCCGGCTCGTGGGA 602

Search completed: March 26, 2003, 14:11:21
 Job time : 412.743 secs

US 097522920MP1



Creation date: 14-08-2003
Indexing Officer: PRT1634 - GAU1634 PRINTER
Team: 1600PrintWorkingFolder
Dossier: 09752292

Legal Date: 12-08-2003

No.	Doccode	Number of pages
1	CTNF	9
2	DIST	1
3	SRFW	1

Total number of pages: 11

Remarks:

Order of re-scan issued on